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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                               1344157 seqs, 7733874588 residues
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                                                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AX063767 Sequence	X96471 C.glutamicu	A93933 Sequence 2	AL357613 Streptomy	U34849 Mycobacteri	I86263 Sequence 17	Z74025 Mycobacteri	AB011413 Streptomy
!	ID	AX063767	CGLYSEG	A93933	SCSF8	MBU34849	186263	MTCY39	AB011413
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4	Score	873	873	873	140.6	122.6	122.6	121	108.6
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X73026 E.coli gene
M62865 E.coli chro
X66836 E.coli sera
AE000375 Escherich
AE00521 Escherich
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141665 Synechococc
AE004639 Pseudomon
AB053349 Synechoco
AY017305 Synechoco
AX3817 Poutida ca
AL008883 Mycobacte
AE004736 Pseudomon
AE004566 Escherich
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AL162755 Neisseria
AP003003 Mesorhizo
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1 (bases 1 to 993)
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G. corynebacterium glutamicum genes encoding metabolic pathway
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AP002563 Escherich
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BASF AKTIENGESELEGHAFT (DE)
Location/Qualifiers
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Corynebacterium glutamicum
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954 ATGAACCCCATTCAACTGGACACTTTGCTCTCAATCATTGATGAAGGCAGCTTCGAAGGC 895
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                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
Location/Qualifiers
                                                                                                                                                                                                       Variation, Sahm, H. and Eggeling, L.
A new type of transporter with a new type of cellular function:
L-lysine export from Corynebacterium glutamicum
Mol. Microbiol. 22 (5), ,815-826 (1996)
97126810
                                                                                 Lysine
                                                                           lysE gene; lysG gene; Lysine export regulator protein; exporter protein; Lysine governor.
Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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/db_xref="G1:1729756"
                                   genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Lysine governor"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1723. .2352)
/gene="orf3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1723. .2352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="lysg"
complement(82. .954)
                bp DNA
and lysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDAVVDAAIEGLRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1025. .1726
/gene="lysE"
1025. .1726
/gene="lysE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="orf3"
                                                                                                                                                                                                                                                                                    2 (bases 1 to 2374)
Vrljic, M.M.
                                                                 GI:1729753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="lysG
                                                                                                                                                                                             (bases 1 to 2374)
                              C.glutamicum 1
X96471
X96471.1 GI:1
                              DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                ORGANISM
                                                                                                                                                                                                            AUTHORS
TITLE
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 CGLYSEG/c
                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                          REFERENCE
                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                                                                                              SOURCE
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355

099 295 720 235 780 175

Oy 721 gctcccat Db 234 GCTCCCAN OY 781 atgtattc OY 781 atgtattc OY 841 gttgatgc OY 841 gttgatgc Db 114 GTTGATGC CCOS DEFINITION Strept ACCESSION AL3571	Σ	REFERENCE 2 (be AUTHORS Seeger JOURNAL Unpubl REFERENCE 3 (bs AUTHORS Thomso TITLE Direct JOURNAL SUBmit COMMENT SANGEL COLORS C	stranc The mc The le Usuall Cusuall Cusuall Where Gene F Gene F Gene F Griff Nuclei Progra http://
	.;0		
A93933 A93931. GI:6742037 Corynebacterium glutamicum. Gorynebacterium glutamicum. M Corynebacterium glutamicum. Bacteria, Firmicutes; Actinobacteriae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. Torynebacterium. Actinomycetales; Corynebacteriaes; Corynebacterium. Torynebacterium. Torynebacterium glutamicum" ACTIVITY OF EXPORT CARRIERS PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS BY BOOSTED ACTIVITY OF EXPORT CARRIERS PROTIVITY OF EXPORT CARRIERS PROTIVITY OF EXPORT CARRIERS PROTIVITY OF EXPORT CARRIERS PROTIVITY OF CARONICA JUL-1997; RERNFORSCHWASANIAGE JUELICH (DE); VRLIJC MARINA (DE) LOCATION/Qualifiers 12374 AD_XTGF="Laxon:1718" AD_XTGF="Laxon:1718" AD_XTGF="Laxon:1718" AD_XTGF="Laxon:1718" AD_XTGF = ACTION	tch al Similarity 100.0%; Score 873; DB 9; Length 2374; al Similarity 100.0%; Pred. No. 1.1e-235; 873; Conservative 0, Mismatches 0; Indels 0; Gaps atgaaccccatcaactgacactttgctcctcaatcattgatgaaggcagcttcgaaggc 11	gaagtccttgtgcaagcagcggaaaatggtgttgctgcaagcagaaactaaagcgcaa 240	cacttggccattgcaacccctcattgcgggatgcctacatggttgatgggaaactagat 540
ACCESSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL FEATURES SOUIC	ORIGIN Query Match Best Local S Matches 873 QY 1 1111 Db 954 ATGA QY 61 gcctr QY 121 catc QY 121 catc	0.9 181 0.0 7.74 0.9 241 0.9 301 0.0 654 0.9 361 0.0 594 0.0 534	0y 481 Db 474 Qy 541 Db 414 Qy 601 Db 354 Oy 661

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Struauu, The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Saually the highest scoring match found by fasta -o is given for EDS which show significant similarity to other CDS in the database. The postition of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Sene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Walceler, Acids Research, 22(22):4768-478(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at Ittp://www.nh.go.jp.

Ittp://www.nh.go.jp.

Ittp://www.nh.go.jp.

Ittp://www.nh.go.jp.

Oddon (atg, gtg, ttg or (att)) which is preceded by an upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    itted (05-JUN-2000) Streptomyces coelicolor sequencing project, er Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge ISA E-mail: Barrell@sanger.ac.uk Cosmids supplied by Prof. A. Hopwood, [3] John Innes Centre, Norwich Research Park, ey, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
pases 1 to 33285)
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"http://www.sanger.ac.uk/Projects/S_coelicolor/) are numbered using the following system eg SC/B7.01c. SC (S. are numbered using the following system eg SC/B7.01c. All icolor), 7B7 (cosmid name), .01 (first CDS), c (complementary nd).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7,7613.1 GI:8347023
no acid decarboxylase; anti-sigma factor; integral membrane lean; LuxR-family regulator; LysR-family transcriptional lator; membrane transport protein; oxidoreductase; regulatory lator; membrane transport protein; oxidoreductase; regulatory lator; RNA polymerase sigma factor; serine/threonine protein ise; stress-inducible protein; TetR-family transcriptional lator; thioredoxin reductase; threonine dehydratase; component sensor histidine kinase.

pytomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Shi, H. and Hopwood, D.A.

t of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                           09-JUN-2000
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son, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
ct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                             8 33285 bp DNA ptomyces coelicolor cosmid 5F8.
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blished
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FEATURES

CDS

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/note="SC5F8.03c, unknown, len: 225 aa. Similar to several proteins of undefined function including: Deinococcus radiodurans TR:09RWP1(EMBL:AB001920) conserved hypothetical protein (254 aa), fasta scores opt: 467 z-score: 555.6 E(): 1.8e-23 36.6% identity in 205 aa overlap and Straptomyces coellicolor TR:CAB70638(EMBL:AL13742) SCBF4.12C (239 aa), fasta scores opt: 397 z-score: 474.2 E(): 6.1e-19 36.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKGDLFSSEHMVQPATAPGMTVENSKCIRYAVNGEMLARQGAMJ
XRGNLQFBERKGGGVGGMLKRAVTGEGLPLMAVRGGGBAMFARRAQNCTVVEVPEPGDE
FTVNGRNVLCFDASLSYRIAVRKGSGIAGGGLFNSVRTGGGRLGLVCBCNPLVIPVSQ
OYPVHVDTDAVVGWSAGLATSLHRSQSIGSMLRGGSGGAVQLVLQGGGFVVVRPSEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SCFFB.O4c, unknown, len: 434 aa. Similar to
Streptomyces coelicolor TR:09X9W9(EMBL:AL096743) putative
transport associated protein, SCI7.21 (399 aa), fasta
scores opt: 428 z-score: 449.2 E(): 1.5e-17 38.3% identity
in 209 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTHAGWACVTGGPSGDTYWTALWAVPLTPDGLARTTAEVVGLTNRERAGAGLPALAVD
ARLTAAAQAHSADMVTRDFYSHTDPDGGKPWDRAAAAGADRRSVGENIACGQRSPAEV
VEGWMNSPGHRANILEAGFTHIGVGLAGGGRAGTYWTQLLGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3562..6528)
/gene="SCSF8.05c"
complement(3562..6528)
/gene="SCSF8.05c"
/gene="SCSF8.05c"
/note="SCSF8.05c"
/note="SCSF8.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aa. Similar to several other putative regulators from Streptomyces coelicolor including:
TR:QYXAM (FUMBL:ALO79355) SC4G6.06 (893 aa), fasta scores opt: 305 2-score: 328, TE(): 7, 7e-11 26.48 identity in 910 aa overlap and TR:Q92573(EMBL:ALO35569) SC8D9.18 (1091 aa), fasta scores opt: 857 2-score: 926.1 E(): 0 36.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identity in 1077 as overlap. Contains a Prosite hit to PS00017 ATP/GTP-binding site motif A (P-loop) Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLLRFLLGRGVLQRPAGGAPGHRLALFASYRADDLHRRHPLRPLLAELVRLPGVERLE
LRPLPDSDVARLVRLLRERRLPDSTVRRIVERAEGNAFYAEELVAATDAPAGGVPSGL
ADVLLIRFEQLSETAQOVLRTAAVAGRRVGHDLLRDAVGLPEEELESALREAVERQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSDLVPGGNVPLPGGPVSVRVPGGFDVSALVTDEGGKVGGDADF
VFYNQPEAPGARLRDDTLTVDPARLRRGAARVTVAVGPSDPGTPLGALPSPTVLVTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGRTVARFTPARPGRETVLLLVEFYRRGEGWKVRALGQGYADGLAGLARDFGVEVTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPEPATAPEPLTPGADSDGFLNLVNSARAAGSPAVRPDPRLRSAARAHAAAMAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLSIETRDGVSVHQRVVSAGFAYLTVGEHLVSGPRTPAEFVAYCLRAERTRRTLHDTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MGGVPQTSLTSPLVGREDELARLTGVLERARAGEARAVLVAGDA
GVGKTRTLHEAAGRAAAAGTTVLTGHCVDLGDVGLPYLPFTEILGVLAADERFAAVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHPVADRLLGGGPDDGTDAAPSRLRLFEGVAALLTELADVAPLLLVLEDLHWADQSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 140.6; DB 3; Length 33285; Pred. No. 6.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein SCSF8.03c."
/protein_id="Cab93731.1"
/db_xref="G1:8347026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein SC5F8.04c."
/protein_id="CAB93732.1"
/db_xref="GI:8347027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative LuxR-family regulator." /protein_id="CAB93733.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                     identity in 183 aa overlap.'/codon_start=1
                                               complement(1477. .2154)
/gene="SC5F8.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC5F8.04c"
complemen+')'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2166. .3470)
/gene="SC5F8.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%;
50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POKPOOH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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/gene="SCSFB.02c"
/fote="SCSFB.02c"
/fote="
ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase, partials CDS, len:> 114 aa. Similar to many proposed Streptomyces coelicolor serine/threonine protein kinases e.g. TR:CAB82014(EWBL:AL161755) SCD63.07 (717 aa), fasta scores opt: 172 z-score: 222.0 E(): 6.8e-05 33.0% identity in 103 aa overlap. Overlaps and extends into CDS SCSH.01 on the adjoining cosmid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARSVEIAEEBGALVRLIDGMDSAFALVTRLREEGLTLVHPFDDPVVVAGQGTVGLEF
BEDASDLTDVLVSIGGGGLIAGVAAALRALRPGVRVWWGYEGABAMSRALAAGGPLT
VPLSSVYTTLSAPSVSRLTYDHVAELVTEVLVVPDRRAVRGSIALAEHAKVWTEPAAG
CLLPAARRVVERVGDGARIGLVVCGGNATVGDMAVWADRFGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MIAITEIEAAAERIAGHVVRTPTVPSPGLSALLGVPVTAKLELL
QRTGSFKARGATAKLLSLTEAERAAGVVAVSGCNHGIAVAVMAAALDVKATVVMPRTA
                                                                                                                                                                                                 overlapping sections once, or longer, because we arrange for a mail overlap between neighbouring submissions.
Cosmid 5F8 lies on genomic restriction fragment Asel-A bordered by cosmids 5H1 and 4G10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1. .108)
/gene="SC5F8.01c"
/note="nominal overlap with cosmid SC5H1 between bases
                                                                                                                            IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note "SC5F8.01c, possible serine/threonine protein
                                                                                                                                                                       It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="fam match to entry PF00291 S_T_dehydratase,
Pyridoxal-phosphate dependent enzyme, score 210.10,
E-value 3.3e-59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative serine/threonine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00165 Serine/threonine dehydratases
pyridoxal-phosphate attachment site"
complement(1477. .2154)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1287. .1328)
/gene="SC5F8.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(492. .1451)
/gene="SC5F8.02c"
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/gene="SC5F8.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SC5F8.01c"
complement
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1. 33285
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CDS

Actinobacteria; Actinobacteridae;

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Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                 source
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                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17612 CCCTGCGCCCCCGAGTTCGCCGCCCGGCATCTGGACGCCCCGCTGCGGGAGACGGTC 17553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17492 CGGCTCGGTCACGGTGGCGCCGCCGCACGCCATTAC---GTGCCGACCTCGGAGGGC 17436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17315 CTGTACTGGCAGCAGTGGAAGCTCGACTCCCGGCGCTGGCCACGGTGGCGGACGCGGTG 17256
                                                           18092 CAGGTGCGCACCCTGCTGGCCGTCGTGGACGAGGGCACCTTCGACGCGGCGCCGCCGCCGCC 18033
                                                                                                                                                                                                                                              17912 CGGCTGGCCCGCCAGGTGGCGGGCTGGAGCGGGACGCCTCGGCCCGAGCTGGGCCTGCGG 17853
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                             caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc
                                                                                                                                                       cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                                                                                                                                                             253 cttgctg-----aaatcccgttaaccatcgccatcaacgcagattcgctatccacatgg
                                                                                                                                                                                                                                                                                                                                           tttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctgcgcttg
                                                                                                                                                                                                                                                                                                                                                                        17792 TrccrGcccGcccrcAcccGCGATCCGGGGGAGCCCGCACTCTGGTTCGAACTGCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                      gaagatgaagcgcacacattatccttgctgcggcgtggagatgttttaggagcggtaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 gctgcgatgcccgtcttacgcttcggtcccaaagatgtgcttcaagaccgtgacctggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccatgctaaaagcaggagaagtgatcctccg---atgagatacccattgacacacg
 15;
 Mismatches 414; Indels
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Conservative
Matches 444;
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immunogenic protein (mpt64)

U34849.1 GI:1049224 Mycobacterium bovis. Mycobacterium bovis

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

DEFINITION

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/translation="MRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSDPAXNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQS
AIPPRGTQAVVLKVYQNAGGTHPTTTYRAFDWDQAYRKPITYDTLWQADTDPLPVVFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVQGELSKQTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFFNPGELLPEAAGPTQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .14844
//Organism="Mycobacterium bovis"
//Organism="Mycobacterium bovis"
//Organism="mycobacterium bovis"
2864. .2888
//Note="one of two imperfect direct repeats located at or near the deletion breakpoints"
//Note="this interval is completely absent in the closely rolated, but avirulent strain Mycobacterium bovis BCG"
//gene="mpt64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or
                                                                                                                                                                                                                                                                                                                                           and Stover, C.K.
                                                                                                                                                                                                       Stover, C.K.
                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                               Mycobacterium
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium: Mycobacterium tuberculosis complex.
1 (bases 10567 to 11392)
Oettinger,T. and Andersen,A.B.
Cloning and B-cell-epitope mapping of MPT64 from Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13652.
7note="one of two imperfect direct repeats located
near the deletion breakpoints"
4682 c 4603 g 2759 t
                                                                                                                                                                                                                                                                                                                                    Mahalras,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stoves
Direct Submission
Submitted (24-AUG-1995) Mark J. Hickey, Molecular Micro.,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4979 CAGGTGCTGGTGGTCAGGGAAAAGCCATGTCGGGCGACGACGCAGGTATCCCGCTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14844;
                                                                                                                                                                                                          and
                                                                                                                                                                         Mahairas, G. Sabo, P. J., Hickey, M. J., Singh, D. C. Mahairas, G. G., Sabo, P. J., Hickey, M. J., Singh, D. C. Molecular analysis of genetic differences between bovis BCG and virulent M. bovis J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 122.6; DB 3;
Pred. No. 8.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 8.4e-24;
0; Mismatches 409;
                                                                                                                              Infect. Immun. 62 (5), 2058-2064 (1994) 94222581
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/note="immunogenic
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
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Mycobacterium tuberculosis H37Rv complete genome; segment 89/162. 274025 AL123456 Z74025.1 GI:3261586
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                                                                                                                                                                                                                                                                                         tttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctgcgcttg 366
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1 (bases 1 to 38500)

1 (bases 1, Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctttccatttccccttcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
                                                                                                                                                                        gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
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                                                                                                                CAGGTGCTGGTGGTCAGGGAAAAGCCATGTCGGGCGACGACGCAGGTATCCCGCTGTTG
                                                                                                                                                      caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                                                                                                                                                                                                                                                                                                                                        gaagatgaagcgcacattatccttgctgcggcgtggagatgttttaggagcggtaacc
                                                                                                                                                                                                                                                                                                                                                                                           5604 GAGGACCAGGACCATTCCGCGCGGCTGCTACGGGAGGGTGTGGCCGATGGGCGCGGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                               cgtgaagctaatcccgtggcgggatgtgaagtagaacttggaaccatgcgccacttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gocattgcaacccctcattgcgggatgcctacatggttgatgggaaactagattgggct
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Stover, C. Kendall and Mahairas, G.G.
Virulence-attenuating genetic deletions deleted from mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                     CGTAAGGCCTTTCGTCGCGCCATCACCAGACCGACGTTTGTCCCGACCACAGAGGGC 5509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5253 CAGCTGGCCGCATTGGCTGCCGTGGTCGAACTGGGCAGCTTCGATGCGGCCGCGGAGCGC 5312
                                                                                  TTTTCGGCCGTGTTCGACG-----GTCTCGGCGACGTCCTGCTCGACGTTCGGATC 5209
                                                                                                                                                                                                                     5270 ACCGAGCGGAACCCGGTGCCGGGCTGCCGGTGCACCCGCTGGGTGAATGCGCTACCTA 5329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgtgaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgcgccacttg
                                                                                                                                                                                                                                                                                                                           gegatgeeegtettaegetteeggteeeaaagatgtgetteaagaeegtgaeetggaeggg
                                                   ttcctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctgcgcttg
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Pred. No. 8.4e-24;
0; Mismatches 409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 from patent US 5700683.
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a 4791 c 4729 g
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illarity 49.9%;
Conservative
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| GCGCGCCAAGCG 5702
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AUTHORS TITLE JOURNAL

COMMENT

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REMARK

JOURNAL

TITLE

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2981...2985

/note="ggag9, potential rbs upstream of Rv1983"

2992...4668

/gene="PE_PGRS"

2992...4668

/gote="PE_PGRS"

/note="Rv1983, (MTCX39.36C), len: 558; Member of M.

/mCX130.10C, (43.3% identity in 522 aa overlap)"
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/protein_id="CAA98400.1"
/db_xref="G1:140472"
/db_xref="G1:140-472"
/
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/gene="Rv1982c"
/note="Rv1982c, (MTCY39.37), len: 139. Similar to
Mycobacterium tuberculosis Z92772|MTY20H10_5 (131 aa)
FASTA scores: opt: 288 z-score: 388.5 E(): 4.1e-14; 40.28
identityin 127 aa overlap, also similar to Rv2759c, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MIVDTSAVVALVQGERPHATLVAAALAGAHSPVMSAPTVAECLI
VLTARHGPVARTIFERLRSEIGLSVSSFTAEHAAATQRAFLRYGKGRHRAALNFGDCM
TXATAQLGHQPLLAVGNDFPQTDLEFRGVVGYWPGVA"
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ADHREYTCELLHTLYANEIDYAHDLYDELGWTDDVLPYMRYNANKALANLGYQPAFDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTGKLVERVHAINWNRLLDAKDLQVWERLTGNFWLPEKIPLSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LASWQTLSSTEQQTTIRVFTGLTLLDTAQATVGAVAMIDDAVTPHEEAVLTNMAFMES
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YYIEATYTTVDFGNGIVTAPTANVNVLLSIPTSPFALSTEYSALLAPPTTPPERAYF
GAGVOGVLGVGPNAVGFBIPTMALPGDLNGGVLIDAPAGELVFGPNPLPAPNVEV
GSPTTTLYVKIDGGPPIPVPBIIDSGGVTGTPSYVLGSGTLFANTNIEVYTSPGGD
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small subunit, len: 322, highly similar to RIR4_SALTY P17424, ribonucleoside-diphosphate reductase (319 aa) FASTA scores, opt: 1402, ~scores: 1716.0, E(): 0, (66.0% identity in 315 aa overlap); Also similar to RV3048c, (MTV012.63c): containsPS00368 Ribonucleotide
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complement(2161. .2580)
/gene="Rv1982c"
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/protein_id="cAp8401.1"
/bx.ref="G1:1403473"
/db_xref="SWISS-PROT:Q10874"
                                                                                                                                                                                                                                   reductase small subunit signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SWISS-PROT:Q10840"
                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA98381.1"
/db_xref="GI:1403474"
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced g1:1403436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSDPAYNINISLPSYYDDQKSLENYIAQTRDKFLSAATSSTPREAPYENITSATYOS
AIPPRGTQAVVLKVYQNAGGTHPTTTYKAFDWDQAYRKPITYDTLWQADTDPLPVVFP
IVQGELSKQTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFFNPGELLPBAAGPTQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position g + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome blinding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQ
                                         Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squres, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Rv1960c, (MTCY39.39), len: 228. mpt64 identical to
MPB6_MYCBO P19996 immunogenic protein mpb64/mpt64 (228
ab. Similar to Rv3036c, (MTV012.51c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(968. .1936)
/gene="nrdf"
/note="Rv1981c, (MTCY39.38), ribonucleotide reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                  Deciphering the biology of Mycobacterium tuberculosis from the
         Basham, D., Brown, D., Chillingworth, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(787. .791)
/note="ggagg, potential rbs upstream of Rv1980c"
complement(968. .1936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erratum:[[published errâtum appears in Nature 1998 Nov
12,396(6707):190]]

    .38500 /
/organism="Mycobacterium tuberculosis"

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/strain-"H37Rv"
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/protein_id="CAA98382.1"
/db_xref="G1:103475"
/db_xref="SWISS-PROT:P19996"
                                                                                                                                                                                                                                                                                                                                                            complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available on the World Wide Web.
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    Tekaia, F., Badcock, K.,
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(bases 1 to 38500)
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Actinomycetales; Streptomycineae; Streptomycescaese; Streptomyces.
1 (bases 1 to 12070)
    427 cgtgaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgggcacttg 486 6212 Accadagaccactgggaccacttg 486 6212 AccadagcacaccgcTgcCacccgcTgGCTGAATGCGCTACGTA 6153
                                                                                                                                                                                                                                                                                                                     5973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5853
                                                                                                                                                                                                                                                                                                                                                                                                6092 GCGGCTAAAAGCTCCGTCACTGGCGTGGAATCGTGACGATGGGCTGCAGGACATGTTGGTG 6033
                                                                                         546
                                                                                                                                                                                                                                                                                                                                                                  664 tttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgct 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                           724 cccatgctaaaagcaggagaagtgatcctcctcgatgagatacccattgacacaccgatg 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-FEB-1998) to the DDBJ/EMBL/GenBank databases. To Umeyama, University of Tokyo, Department of Agriculture and L. Sciences: Yayoi 1-1.1, Bunkyo-ku, Tokyo 113, Japan (E-mail:aa67103@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-3812-2111)
                                                                                                                                                                                                                                                                             cg---cgtcgatggtcctgtgggggggggggggtatccattgtcccgtcgggggaggt
                                                                                                                                    6152 CCAGTGGCCAGCAGGCCATTCGTCCAGCGCCCATCTATCCGACGGGTTCACTGCCGCGGG
                                                                                                                                                                                                                                                                                                  6032 CGTAAGGCCTTTCGTCGCCGCCATCACCAGACGACGCACTTTGTCCCGACCACAGAGGC
                                                                                            gccattgcaaccccctcattgcgggatgcctacatggttgatgggaaactagattgggct
                                                                                                                                                                                   547 gegatgecegtettaegetteggteecaaagatgtgetteaagaeegtgaeetggaeggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5912 TCTCCGCTTGCCGATGGATCGTTCGTACGGGTCTGCGACATACACCTCGACGTCCCTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Open reading frame encoded around afsA gene
Unpublished (1998)
Location/Qualifiers
1. 12070
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complement(2660..3511)
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/gene="orf2"
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Streptomyces griseus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:3401946
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TITLE
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                                        /note="Rv1984c, (MTCX39.35), len: 217. Probable cutinase precursor with N-terminal signal sequence, , similarity to CUTI_ALTBR P41744 cutinase precursor, (209 aa) FASTA scores, opt: 283, z-score: 322.0, E(): 2.2e-11, (32.6% identity in193 aa overlap). Also similar to M. tuberculosis Rv3452, Rv3451, Rv2301, Rv1758, Rv3724."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jote="Rv1985c, (MTCX39.34), len: 303, LysR family member similar to many regulatory proteins, especially ICIA_ECOLI P24194, chromosome initiation inhibitor, (297 aa), and P94632 LYSINE EXPORT REGULATOR PROTEIN (290 aa). FASTA scores, P94632 LYSINE EXPORT REGULATOR PROTEIN opt: 705 z-score: 850.6 E():
                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:Q10837"
/translation="MTPRSLVRIVGVVVATTLALVSAPAGGRAAHADPCSDIAVVFAR
                                                                                                                                                                                                                                                                                                                                        GTHQASGLGDVGEAFVDSLTSQVGGRSIGVYAVNYPASDDYRASASNGSDDASAHIQR
TVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVADHVAAVALFGEPSSGFSSMLWGGG
SLPTIGPLYSSKTINLCAPDDPICTGGGNIMAHVSYVQSGMTSQAATFAANRLDHAG"
complement(4950, 4967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overlap; and ICIA_ECOLI P24194 opt: 520, Z-score: 632.5, E(): 1.1e-28, (35.8% identity in 285 as overlap); contains PS00044 Bacterial regulatory proteins, lysk family signature. Also contains helix-turn-helix motif at as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6563 CTACATGTCACCCCGTCGGCTGTCAGTCAGCGCATCAAGTCGTTGGAGCAGCAGGTCGGC 6504
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Pred. No. 2.2e-23;
0; Mismatches 410; Indels 18.
                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Rv1984c"
/gote="PS00155 Cutinase, serine active site"
complement(5739. 6650)
                                                                                                                                                                                                   /transl_table=11
/product="hypothetical protein Rv1984c"
/protein.id="CAA98399.1"
/db_xref="GI:1403471"
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/product="hypothetical protein Rv1985c"
/protein_id="CAA98410.1"
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complement(5739. .6650)
/gene="Rv1985c"
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                                                                                                                                                                                                                                                                                                                               73 ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
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         48.8%;
    Best Local Similarity 48.8 Matches 425; Conservative
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/db_xref="G1:340195
ALTGHVLSGRSCGPAWEALEQQERLLADAAHELRTPVAVWRGSVEVAAGAPGGLEGGL
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LEESVVEADAALVRVAVRNLLDNAVRHGPGSRGAAGRGRTAGDRVRTGVRVADRGPAV
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ATAGLQLLSPEPEPGARTTAAGNVLARDAPGTWAMRAWFTDPVMLRGWDLLDESVRT
GETTFDTVFGTDFFGHLRAFPELSAAFNEAWSGGTRLTAETVPHYDFGRFQRLVDIG
GGDGTLLASILRAHQPERGVLEPTAEGLAGAPRRLAREGLDGRYTETGDFFRSAPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MRVLVEDDDDLRDVIGAGLRDGGFAWDCASDWPEADVLLHLSA
POCVVLDRWYPSGDTLAPLEGRRRAGWSVPVLCTALDSLDSERIRGESGADDVLTAKP
FSMRELVLEVRGLSSRRSARLESFLGCADVWMDVARIEVRRGGVLLSLSPKEYAVLOD
LLYHRDTVVTRTGLLEHCWDEMADPVSNVVDAVVGLRRKLGSPGLVHTVRGGGFLLS
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/db_xref="GI:3401951"
/translation="MDAEAEVVHPVGIEMVHRTRPEDAFPRNWVRLGRDRFAVEAVLP
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VGGEPTEIGLEVFCSDLKWRAGLPAQGRVGWAVHRGDRLAATGVAATRFSTPKAYRRM
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I HOARGGWGEGIT WALLY ARTHAN FRANKEL WEED HILLIDER GALLHSU
GREOHCAEGNTOTY NALLDRNGEPTYGGY STHLVVTEK FALS I PEGIALDEAAPLLCAG
THY YSPLEMEWAGAPCKKUNVGLGGIGHMANK TAHALGAEVTYLSQSERKKDOGLKLG
ADHYY ATGOPPTER FENTLESTY FOLLSY SAPLED FGAY LALLKTEGTLNNVGAPEEPVSL
NLF SLILGNRS I AGSAIGGIEF TOWN CANNOGAPEEPVSL
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HVPGMLLLEAARQAACLVAGPAGIVPVEARTRFHRYSEFGSPCWIGAVVQPGADEDTV
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                                                                                                                                                                                                                                 function="two-component regulator protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function-"alcohol dehydrogenase"
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/function="regulator protein"
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/function="methyltransferase"
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/db_xref="GI:3401949"
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/db_xref="G1:3401948"
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                                                                                                                                                                                            complement(3523. .>4197)
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/transl_table=11
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/transl_table=11
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5803

5743

595

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5623

772

715

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5503

ribose phosphate isomerase A. Escherichia coli. Escherichia coli

KEYWORDS SOURCE ORGANISM

Length 12070;

DB 1;

Score 108.6;

12.48;

Query Match

5863

489

ij

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/translation="MKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN MFGQPLLVRTVPRRPPREDGGKLLALLRQVELLEEBWLGDEGTGSTPLLLLSLAVNADSL ATWLLPALAPVLADSPIRLNLQVEDETRQERLRRGEVVGAVSIQHQALPSCLVDKLG ALDYLFVSSR PFABEK FPROVTRSALLKAPVAFDHLDDMHQAFLQONFDLPFGSVPC HIVNSSEAFVQLRAPGATCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOICIA 1815 bp DNA BCT 06-MAR-1995
E.coli chromosome initiation inhibitor (iciA) gene, complete cds.
M62865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

1 (bases 1 to 1815)
Thony, B., Hwang, D.S., Fradkin, L. and Kornberg, A.
icia, an Escherichia coli gene encoding a specific inhibitor of chromosomal initiation of replication in vitro
Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4066-4070 (1991)
91239508
                                                                                                                                     275 tegecateaaegeagattegetatecacatggttteeteeegtgtteaaegaggtagett 334
                                                                                                                                                            335 cttggggtggagcaacgctcacgctgcgcttggaagatgaagcgcacacattatccttgc 394
                                                                                                                                                                                                                                                                                               395 tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg 454
                                                                                                                                                                                                                                                                                                                                         126 TGCGCCGCGGCGAAGTGGTCGCGCGGTGAGTATTCAACATCAGGCGCTGCCGAGTTGTC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="Inhibitor of oric replication in vitro"
/product="chromosome initiation inhibitor"
/protein_id="AAA62780.1"
/db_xref="G1:146436"
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                                                                                               TGCTGGAAGAAGAGTGGCTGGGCGATGAACAAACCGGTTCGACTCCGCTGCTGCTTTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome initiation inhibitor; iciA gene.
E.coli (strain W3110) DNA, (Kohara library) clone IA2
('miniset'-set No. 471).
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62.8 min. on K-12 map; kb coordinate 3974.
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Pred. No. 1.9e-12;
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/map="62.8 min. on K-12 ma"
650. .1543

    1815
    organism="Escherichia"

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/strain="K-12"
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650. .1543
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/gene="iciA"
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Best Local Similarity
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ORIGIN
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TITLE
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KEYWORDS
SOURCE
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ATWLLAPALAPVLADSPIRLNLQVEDETRTQERLRRGEVVGAVSIOHQALPSCLVDKLG
ALDYLFVSSKPFAEKY"
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GIEGAVSSDASTEKLKSLGHHYDDINEVDSLGIYVDGADEINGHWQMTKGGGAALTR
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VTDNGNVILDVHGMEILDPIAMENAINAIPGVVTVGLFANRGADVALIGTPDGYKTIV
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Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                   1 (bases 1 to 1804)
Hove-bensen, B. and Maigaard, M.
Escherichia coli rpilA gene encoding ribose phosphate isomerase
J. Bacteriol. 175 (17), 5628-5635 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 TGATACGTGAACGAGGATTTGAGCGCGCGCGCACAAAAGCTGTGCATTACACAATCAGCCG 427
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                                                                                                                                                                          Direct Submission
Submitted (23-APR-1993) B. Hove-Jensen, Dept. of Biological
Chemistry, Univ. Inst. of Mol. Biology, Solvgade 83, Dk-1307
Copenhagen, DENMARK
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Pred. No. 1.9e-12;
); Mismatches 234; Indels
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protein_id="CAA51509.1"

    1804
    /organism="Escherichia coli"
/strain="K12"

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'db_xref="G1:405639"
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                                                                                                                                                                                                                                                                                                                                                                                                                      complement(<1. .529)
/gene="iciA"
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/codon_start=1
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complement(1. .529)
/gene="iciA"
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/transl_table=11
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/gene="rpiA"
944. .946
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/gene="rpiA"
1 448 c
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/gene="rpiA"
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/gene="rpiA"
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                                                                                                                                     2 (bases 1 to 1804)
Hove-Jensen, B.
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Matches 223; Conservative
                                                                                                                  93374859
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                                     REFERENCE
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/translation="MAKVSLEKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDD
EQLKESIRDAHFIGLRSRTHLTEDVINAAEKLVAIGCFCIGTNQVDLDAAAKRGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATWILPALAPVLADSPIRLNLQVEDETRTQERLRRGEVVGÄVSIQHQALPSCLVDKLG
ALDYLLVSSREPAEKTPROTYRSALLKAPVVAFDHLDDMHQAFLQQNFDLPPGSVPC
HIVBNSSEAFVQLAGGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
RMMRKVTDALLDYGHKVLRQD"
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QHRBNLLAAAVNAARVRATLGEISDALEVAFDRYLVPSQCYTGVIAOSYHQSRKSASE
EDAVVAQTEQFLADNGRRPRILIAKMGQDGHDRGAKVIASAYSDLGFDVDLSPMFSTP
EEIARLAVENDVYVGASSLAAGHKTLIPELVEALKKWGREDICVVAGGVIPPQDYAF
LQERGVAAIYGPGTPMLDSVRDVLNLISQHHD"
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LGGASQRARELMLLCEAAGYDVVIVETVGVGQSETEVARMVDCFISLQIAGGDDLQG
IKKGLMEVADLIVINKDDGDNHTVVAIARHMYESALHILRRKYDEWQPRVLTCSALEK
RGIDEIWHAILDFWRAJAGSRLQOYRQQQSVEWLRKQTRRRSTESFVRE"
1615 c 1550 g 1413 t
                                                                                                                                                                                                                                               /translation="MRVKFHTTGETIMTQDELKKAVGWAALQYVQPGTIVGVGTGSTA
HFIDALGRAKGQIEGAVSSDASTRKLKSLGHHYEDLMBVDSIGIYVOGADEINGHM
QMIKGGGAALTREKITASVARKFICTADARSKOYDILGKFPLPVEVIPMARSAVRQLY
KLGGRPEYRQGVYTDNGNVILDVHGMEILDPIAMENAINAIRGADVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="msnvqewqqiankelsrrektvdslvhqtabgialkplytebdL
DNLEVTGTLEFGLPPYYRGPRATMYTAQPWTIRQYAGSSTAKESNAFYRRNLAAGQKGL
SVAFDIATHRGYDSDNPRVAGDVGKAGVAIDTVEDMKVLFDQIPLDKMSVSWTMNGAV
LPVLAFYIVAAEEQGWTPDKLTGTIQNDILKEYLCRNTYIYTPPRPSMRIIADIIAWGS
GNMPRRNIISISGYHWGEAGANCVQOVAFTLADGIEYIKAAISAGLKIDDFAPRLSFF
FGIGMDLFMNVAMLRAARYLWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN
MFGQPLLVRTVPPRPTEQGQKLLALLRQVELLEEEWLGDEQTGSTPLLLSLAVNADSL
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AGSYYIESLTDQIVKQARAIIQQIDEAGGMAKAIEAGLPKRMIEEASAREQSLIDQGK
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Pred. No. 1.8e-12;
); Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA47311.1"
/db_xref="G1:42945"
/db_xref="SWISS-PROT:P27253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA47312.1"
/db_xref="G1:42946"
/db_xref="SWISS-PROT:P27254"
       db_xref="SWISS-PROT:P08328"
                                                                                                                                                                                                                        /db_xref="SWISS-PROT:P27252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SWISS-PROT:P24194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="inhibitor of c
/protein_id="CAA47310.1"
/db_xref="GI:42944"
                                                                                                                                                                            /protein_id="CAA47309.1"
/db_xref="GI:42943"
                                                                          complement(554. .1249)
/note="orf1"
                                                                                                                                                        /transl_table=11
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/transl_table=11
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/transl_table=11
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/note="sbm orf"
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/gene="iciA"
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/gene="iciA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223; Conservative
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Best Local 9
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ORIGIN
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 6055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993 CTGATTCGCCTATCCGCCTCAACTTGCAGGTAGAAGATGAAACCCGCACTCAGGAACGTC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1053 rececedededaderececececegeagranicaacarcageecrecegagricic 1112
                                                                                                  693 TGATACGTGAACGAGGATTTGAGCGCGCGCACAAAAGCTGTGCATTACACAATCAGCCG 752
                                                                                                                                                   tgagtcagcgcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
                                                                                                                                                                                              753 TCTCACAGCGCATTAAGCAACTGGAAATATGTTCGGGCAGCCGCTGTTGGTGCGTACCG 812
                                                                                                                                                                                                                                                  aaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgggaaaatggtgt 214
                                                                                                                                                                                                                                                                                                872
                                                                                                                                                                                                                                                                                                                                                 tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
                                                                                                                                                                                                                                                                                                                                                                                             873 TGCTGGAAGAAGAGTGGCTGGGCGATGAACAAACCGGTTCGACTCCGCTGCTGCTTTCAC 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcgccatcaacgcagattcgctatccacatggtttcctcccgtgttcaacgaggtagctt 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-1992) I. Roy, University of Cambridge, Dept. Blochemistry, CB2 1QW, UK
2 (bases 1 to 6055)
       Gaps
                                                   94
                                                                                                                                                                                                                                                                                      813 TACCGCCCCCCCCCCCACGGAACAAGGGCAAAAACTGCTGCCGCTGCGCCCCAGGTGGAGT
                                              35 tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttccccctcggcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cttggggtggagcaacgctcacgctgggatgaagatgaagcgcacacattatccttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg
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/protein_id="CAA47308.1"
/db_xref="GI:42942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECSERAICI 6055 bp DNA BCT
Ecoli serA, iclA, sbm genes and two open reading
X66836.1 GI:42941
  Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1113 TTGTCGATAAACTTGGTGCGCTCGACTATCTGTTCGT 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 aagtagtagaacttggaaccatgcgccacttggccat 491
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/note="partial of serA orf"
/codon_start=1
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/clone_lib="lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="K12-38
  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy, I. and Leadlay, P.F. Unpublished
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     Conservative
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223;
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  Matches
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VERSION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined by the E. coli Genome Project at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1744 TCTCACAGCGCATTAAGCAACTGGAAAATATGTTCGGGCAGCCGCTGTTGGTGCGTACCG 1803
                                                                                                                                                                                         1804 TACCGCCCCCCCCCACGAACAAGGCCAAAAACTGCTGGCACTGCCCCAGGTGCAGT 1863
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                                                              tgagtcagcggttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
                                                                                                                                                                                                                                      tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
                                                                                                                                                                                                                                                                                                                       tegecateaacgcagattegetatecacatggttteeteeegtgtteaacgaggtagett 334
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Blattner, F.R.
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Blattner, F.R.
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Plunkett, G. III.
Direct Submission
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University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark Software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu] Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A pubblic version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
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//procein_id="AAC75953.1"
//barsef="G01:1789283"
//translation="krrpdyraldlingvelileberigdrogstrictiosavsoringkolden
MFGOPLLVRTVPPRPTEGGGKLIALINGVEDETREEWIGDEGTGSTPLILISLAVNADSL
ATWLLPRALAPVLADSPTRINLOVEDETRYOPRILKRGEVVGAVS1GHQHGLPSCLYDKLG
ALDYLFVSSRPFARKTPNGYTRSALLKAPVARTDHLDDMHOAFLQONFDLPSCSVPC
HIVNSSEAFVQLARQGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRRAPES
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restriction/modification"
/note="0297; 100 pct identical to ICIA_ECOLI SW: P24194;
CG Site No. 28646"
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complement(9. .40)
/note="factor Sigma70; predicted +1 start at 3057674"
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/note="factor Sigma70; predicted +1 start at 3058751"
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/product="replication initiation inhibitor, binds 13-mers at OriC"
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/protein_id="AAC75954.1"
/db_xref="G1:1789284"
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/gene="iciA"
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DAIMPYCGNTLRLGYTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
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ETY ORAWYDCFISLJGIAGGDDLQGIKKGLMEVADLIVINKDDGDNHTNVAIRHNYE
SALHILRRKYDEWQPRYLTCSALERRGIDETWHAIIDFRTALTASGRLQQVRQOGSVE
WLRKQTEEEVLNHLFANEDFDRYYRQTLLAVKNNTLSPRTGLRQLSEFIQTQYFD"
DNLEVTGTLPGLPPYVRGPRATMYTAQPWTIRQYAGFSTAKESNAFYRRNLAAGQKGL
SVAFDLATHRGYDSDNPRVAGDVGKAGVAIDTVEDMKVLFDQIPLDKMSVSMTWNGAV
LPVLAFYIVAAEEGGVTPDKLTGTIQNDILKEYLCRNTYIYPPKPSMRIIADIIAWCS
                                                                         GNMPRENTISISGYHMGEAGANCVQQVAFTLADGIEYIKAAISAGLKIDDFAPRLSFF
FGIGMDLFMNVAMLRAARYLWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV
IRTTIEALAATLGGTQSLHTNAFDEALGLPTDFSARIARNTQIIIQEESELCRTVDPL
                                                                                                                                                                       RVIVGVNKYKLDHEDETDVLETDNVMVRNEQIASLERIRATRODAAVTAALNALTHAA
QHNENLLAAAVNAARVRATLGEISDALEVAFDRYLVPSQCVTGVIAQSYHQSEKSASE
FDAIVAQTEQFLADNGRRPRILIAKMGQDGHDRGAKVIASAYSDLGFDVDLSPMFSTP
EEIARLAVENDVHVVGASSLAAGHKTLIPELVEALKKWGREDICVVAGGVIPPQDYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Translation="MNLSRRNILIKGIFMSYQYVNVYINKVAVIEFNYGRKLNALSK
VFIDDLMQALSDLNRPEIRCIILRAPSGSRYVFSAGHDIHELPSGGRDPLSYDDPLRQI
TRNIQKFRKPIISWYGGSYWGGAFEMIMSSDLIIAASTSTFSWTPVNLGVPYNLVYGIH
NLTRDAGFHYVKELIFTASPTTARARALAYGILNHYVBYEELEDFTLOMAHHISEKAPL
AIAVIKEELRVLGEAHTMNSDEFERIGGMRRAVYDSEDYQEGMNAFLEKRRPNFVGH"
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AGNULDKONPMCOQIADNVYTFLLQBRAGRIPPEFLPLQSGSGVGNINNAVMARLGENP
VIPPFMATSEVLQESVVHLLETGKISGASASSLITISADSLRKITDNNDYFASRIVLRP
QEISNNPEITRRLGYALNVGLEDIYGHANSTHVAGVDLMNGIGGSGDFERNAYLSI
FMAPSIAKEGKISTVVPMCSHVDHSEHSVKVIITEQGIADLRGLSPLQRARTIIDNCA
                                                                                                                                                   AGSYYIESLTDQIVKQARAIIQQIDEAGGMAKAIEAGLPKRMIEEASAREQSLIDQGK
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VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWLTSGIGNAPTWLLRAKKVIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="putative enzyme; Not classified"
/note="0492; This 492 aa ORF is 46 pct identical (7 gaps)
to 490 residues of an approx. 544 aa protein CATI_CLOKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="putative enzyme; Not classified"
/note="0275; This 275 aa ORF is 30 pct identical (6 gaps)
to 250 residues of an approx. 296 aa protein ECHM_RAT SW:
P14604"
                                                                                                                                                                                                                                                                                                                                                                                                                     /function="phenotype; Not classified"
/note="0331; 100 pct identical to YGFD_ECOLI SW:
P27254(257 aa) but has 25 additional N-ter aa 50
additional C-ter aa; orf2 of X66836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative nucleotide-binding protein"
/protein_id="AAC75955.1"
/db_xref="GI:1789285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative coenzyme A transferase"
/protein_id="AAC75957.1"
/db_xref="GI:1789287"
                                                                                                                                                                                                                                                                            "QERGVAAIYGPGTPMLDSVRDVLNLISQHHD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme"
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/product="putative enzyme
/protein_id="AAC75956.1"
/db_xref="GI:1789286"
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/transl_table=11
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/gene="ygfH"
/note="b2920"
5150. .6628
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                                                                                                                                                                                                                                                                                                                                                 'note="b2918"
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                                                                                                                                                                                                                                                                                                   3335. .4330
/gene="ygfD"
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/gene="ygfD"
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/gene="ygfG"
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/gene="ygfG"
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/gene="ygfH"
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/function="putative regulator; Not classified"
/note="f303; This 303 aa ORF is 25 pct identical (11 gaps)
to 241 residues of an approx. 304 aa protein CYNR_ECOLI
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Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 140
                                                                                                                                                                                                                                                                                                                                                                          /product="putative transcriptional regulator LYSR-type"
/protein_id="AAC75958.1"
/db_xref="G1:1789288"
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Escherichia.
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Maylew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F. R. Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 TGATACGTGAACGAGGATTTGAGCGCGCGCGCACAAAGCTGTGCATTACACAATCAGCCG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgagtcagcgcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 TGCGCCGCGCGAAGTGGTCGGCGCGGTGAGTATTCAACATCAGGCGCTGCCGAGTTGTC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 TCTCACAGGGGATTAAGCAACTGGAAAATATGTTCGGGCAGCCGCTGTTGGTGCGTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGGAAGAAGAGGGCTGGGCGATGAACCAAACCGGTTCGACTCCGCTGCTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttcccctcggcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 aaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgggaaaatggtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cttgggggtggagcaacgctcacgcttggcaagatgaagcgcacacattatccttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 CTGATTCGCCTATCCGCCTCAACTTGCAGGTAGAAGATGAAACCCGCACTCAGGAACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 TACCGCCGCCCCGACGGAACAAGGCCAAAAACTGCTGGCACTGCTGCGCCAGGTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82.6; DB 1; Length 1
Pred. No. 1.7e-12;
0; Mişmatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 aagtagtagaacttggaaccatgcgccacttggccat 491
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complement(6625. .7536)
                                                                                                       .7536)
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Escherichia coli 0157:H7 EDL933
                                                                                                                                        /gene="ygfI"
/function="putative
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EPNRHGARYPSYNTIVGGEOGETHH

EPNRHGARYPSYNTIVGGEONGCILHYTENECEMBOBLVLIDAGCEYGYGADITRT

PPVNGKFTQAQREIDTRYTSLESTSLKLYREGTSILEYTGEVKRYGAGDITRT

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/gene" ygf8"

/note="24246"
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/transl_table=11
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/poduct="orf, hypothetical protein"
/poduct="orf, hypothetical protein"
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/db
                   /note="Residues 1 to 441 of 441 are 99.09 pct identical to residues 1 to 441 of 441 from Escherichia coli K-12 Strain MG1655: B2908"
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ATMIDWRPVVHEMRLFKSPEEIAVLRRAGEITAMAHTRAMEKCRPGWFEYHLEGEIHH
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TRYTNTEQLVFIAALNISYELAQEKAKTRDYAASMEQRIRMLQQTIEQALLEQGRITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="putative enzyme; Not classified" /note="Residues 1 to 182 of 182 are 99.45 pct identical to residues 1 to 182 of 182 from Escherichia coli K-12 Strain MG1655: B2912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="orf; Unknown function"
//note="Residues 1 to 109 of 109 are 100.00 pct identical
to residues 1 to 109 of 109 from Escherichia coli K-12
Strain MG1655: B2910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="orf; Unknown function"
//ntenction="orf; Unknown function"
//note="Residues 1 to 194 of 194 are 100.00 pct identical
to residues 1 to 194 of 194 from Escherichia coli K-12
Strain MG1655: B2909"
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Ribosomal and stable RNAs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="orf, hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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4855. .5184
/gene="ygfE"
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5484. .6032
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5484. .6032
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/gene="ygfA"
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/gene="ygfE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5225. .5408
/gene="ssrs"
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/gene="ssrs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="orf; Unknown function"
/note="Residues 1 to 400 of 400 are 98.75 pct identical to
residues 1 to 400 of 400 from Escherichia coli K-12 Strain
MG1655: B2906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEQRVPEPLAADA
PPQLRVSAINAASEKLLTRLGVWQDILSRRASCYHGMEVWDKDSFGHISFDDQSMGYS
HLGHIVENSVIHYALMNKAQOSSDITLLAPAELQQVAWGENETFLTLKDGSMLTARLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPHLCSIVWSLSPEEAQRMQQASEDEFNRALNIAFDNRLGLCKVESARQVFPLTGRYA
RQFAAHRLALVGDAAHTIHPLAGQGVNLGFMDAAELIAELKRLHRQGKDIGQYIYLRR
YERSRKHSAALMLAGWQGFRDLFSGTNPVKKLLRDIGLKLADTLPGVKPQLIRQAMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Menaquinone, ubiquinone di protectione de la constanta de la c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCSLVWCHPLERREEVLSWSDEKFCRELQSAFGWRLGKITHAGKRSAYPLALTHAARS
ITHRTVLVGNAAQTLHPIAGGGFNLGMRDVWSLAETLTQAQERGEDMGDYGVLCRYQQ
RRQSDREATIGVTDSLVHLFANRWTPLVVGRNIGLMTMELFTPARDVLAQRTXGWVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGADGANSWLRNKADIPLTFWDYQHHALVATIRTEEPHDAVARQVFHGEGILAFLPLS
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FDGRAIALAAGTCQQLARIGVWQSLADCATAITTVHVSDRGHAGFVTLAAEDYQLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQVVELHNVGQRLFALLRKAPGVTLHCPDRVANVARTQSHVEVTLEGGETLTGRVLVA
ADGTHSALATVCGVDWQQEPYEQLAVIANVATSVAHEGRAFERFTQHGPLAMLPMSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macromolecule degradation: Degradation
                                                                                                                                          2 (bases 1 to 10367)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Posta, G., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Postai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Mach, R.A. and Blattner, F.R.
Direct Submission
Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="enzyme; Biosynthesis of cofactors, carriers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            col1 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="2-octaprenyl-6-methoxyphenol-->
2-octaprenyl-6-methoxy-1, 4-benzoquinone"
/protein_id="AAG58034.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="orf, hypothetical protein"
/protein_id="AAG58033.1"
/db_xref="G1:12517436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins, peptides, glyco'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="enterohemorrhagic"
complement(357. .1559)
Nature 409 (6819), 529-533 (2001)
21074935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .10367
/organism="Escherichia
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/gene="visC"
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/function="enzyme;
of proteins, peptid
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/note="Z4244"
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MEDLINE
                                                                                                            PUBMED
REFERENCE
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JOURNAL
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RESULT 14
GELDTOPLIEQXWRAGKRVYLPVLHPFSAGNLLFLNYHPQSELVMNRLKIHEPKLDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MAKVSLEKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQLKESIRDAHFIGLRSRTHLTEDVINAAEKLVAIGCFCIGTNQVDLDAAAKRCIPVF
NAPFSNTRSVAELVIGELLLLLRGVPEANAKAHRGVWNKLAAGSFFBARGKKLGIIGYG
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                          DVLPLSRLDVLITPLVAFDEYGQRLGMGGGFYDRTLQNWQHYKTQPVGYAHDCQLVEK
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                                                                          6267. .6659
/note="0-island #118; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="enzyme; Amino acid biosynthesis: Serine"
/note="Residues 1 to 410 of 410 are 100.00 pct identical
to residues 1 to 410 of 410 from Escherichia coli K-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGTCGCGGCGAAGTGGTCGGCGCGGTATTCAACATCAGGCGCTCCCGAGTTGTC 9805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9566 TGCTGGAAGAAGAGTGGCTGGGCGATGAACAAACGGTTCGACTCCGCTGCTGCTTTCAC 9625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9626 TGGCGGTCAATGCCGACAGTCTGGCGACGTGGTTGCTTCCGGCACTGGCTCCTGTATTGG 9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttccccctcggcgg 94 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 tgagtcagcgcttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9446 TCTCACAGGGCATTAAGCAACTGGAAATATGTTCGGGCAGCCGCTGTTGGTGGTGCGTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 aaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgggaaaatggtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tegecateaaegeagattegetatecaeatggtteeteeegtgtteaaegaggtagett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9506 TACCGCCCCCCCCCACGAACAAGGCCAAAAACTGCTGCCCCTGCCCCCAGGTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca
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complement(6814. .8046)
                                                                                                                                                                                                                                                      /function="orf; Unknown function"
/note="No significant matches"
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/gene="24250"
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Consensus quality: 319973 bases at least Q40*
Consensus quality: 373739 bases at least Q30
Consensus quality: 373739 bases at least Q30
Consensus quality: 377379 bases at least Q30
Consensus quality: 37200 bases at least Q20
Estimated insert size: 180000; pulse field gel estimation
Quality coverage: 10.25 in Q20 bases; pulse field gel estimation
Quality coverage: 4.32 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 179 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 29, 2000 Lis sequence version replaced gi:6980223.
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                               AC020850 444882 bp DNA HTG 12-JUL-2000
Mus musculus clone RP21-460J8, WORKING DRAFT SEQUENCE, 179
                                LOCUS AC020850 Accession AC020850
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Center clone name: RPCI-21_460J8
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AC020850_1
AC020850_3
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AC020850_4
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in length

60981: contig of 1175 61081: gap of unknown 62213: contig of 1132 62313: gap of unknown 63704: contig of 1391 65523: contig of 1719 65623: gap of unknown 66821: contig of 1719 66921: gap of unknown 66921: gap of unknown 67957: contig of 1198	69361 709461 709461 722136 722136 73964 75921 75921 76421 76	1 De the control of t	Ouery Match 9.5%: Score 82.6; DB 66; Length 110000; Best Local Similarity 48.8%; Pred. No. 1.5e-12; Matches 223; Conservative 0; Mismatches 234; Indels 0; Gaps 0; Qy 35 tcattgatgaaggcagcttcgaaggcgctccttagcctttccatttcccctcggcgg 94
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11762: gap 13127: conf 13227: gap 14743: conf 16088: conf 16188: gap 17328: conf 17428: gap 18672: conf	20072: gap of unknown length 21352: contig of 1280 bp in 22678: contig of 1286 bp in 22678: gap of unknown length 22678: gap of unknown length 23972: contig of 1194 bp in 24072: gap of unknown length 2586: contig of 1514 bp in 2586: contig of 1514 bp in 26748: contig of 162 bp in 26748: contig of 168 bp in 26933: gap of unknown length 27933: contig of 168 bp in 28033: gap of unknown length 29541: contig of 1508 bp in 30565: contig of 1508 bp in 31222: contig of 1324 bp in 32222: contig of 1157 bp in 32322: contig of 1157 bp in	i unknown length and funknown length and funkn	

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                                                                                                                                complement (559.
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LITQAGGRAFVLQADISDENQVVAMFTAIDQHDEPLAALVNNAGILFTQCTVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA this sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determinations are annotated. This entry should be considered somewhat provisional; it will be updated and merged with others at a later
                                                                                                                                                96669 rGGCGGTCAACGCCGACAGTCTGGCGACGTGGTTGCTTCCTGCACTGGCTCCTGTGTTGG 96610
                                                                                                                                                                                                                                                                                                            96729 TGCTGGAAGAAGAGTGGCTGGGCCGATGAACAAACCGGTTCGACTCCGCTGCTGCTTTCAC 96670
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                      tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
                                                                                                         tegecateaaegeagattegetateeaeatggttteeteeegtgtteaaegaggtagett 334
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                                                                                                                                                                                                                                       96609 CTGATTCGCCTATCCGCCTCAACTTGCAGGTAGAAGATGAAACCCGCACTCAGGAACGTC
                                                                                                                                                                                                                                                                                 tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg
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/note="similar to GenBank Accession Number D21144
(ECOPYUI8)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECU28377 141744 bp DNA BCT
Escherichia coli K-12 genome; approximately 65 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="approximately 65 to 68 minutes"
                                                                                                                                                                                                                                                                                                                                                                                                                 96489 TTGTCGATAAACTTGGTGCGCTCGACTATCTGTTCGT 96453
                                                                                                                                                                                                                                                                                                                                                                          455 aagtagtagaacttggaaccatgcgccacttggccat 491

    141744
    organism="Escherichia coli"

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/db_xref="GI:882432"
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/db_xref="taxon:562"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
1 (bases 1 to 87107)
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Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plunkett, G.
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TITLE
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VERSION
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ECU28377
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QIEGMITROGAVSAAPFGSASILPISWWYIRWGGAEGLKKASQVAILNANYIASRLQD
AFPVLYTGROGRVAHECILDIRPLKEETGISELDIAKRLIDYGFHAFTWSFPVAGTLM
YEPTESESKVELDRFIDAMTAIRAEIDQVKAGVWPLEDNPLVNAPHIQSELVAEWAHP
YSREVAVFPAGVADRYKWPTVKRLDDVYGDRNLFCSCVPISEKQ"
complement(3551. .3940)
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NDAQRQAVBGMKPFFGVQAGDLFIATTGYTGERGYEIALPNBKAADBWRALVEAGVKP
CGLGARDTLRLEAGMNLYGQBMDETIATBPLAANMGWTIAWEPADRDFIGREALEVQREH
GTEKLVGLVWTEKGVLNBLEVPRTDAQGNOHEGIITSGTFSPTLGYSIALARVPEGI
GETAIVQIRNREMPVKVTKPVFVRNGKAVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGYGGPHAAFFAAKDEYKRSMDGRIIGVSKDAAGNTALRMAMÖTREQHIRREKANSNI
CYSQVLLANT NASLYAYYHGYGLKRINKIHRLIDILAAGLOQKGKLKRHSHAYPDTLG
VEVADKAGYLTRAAARINIRSDILANVGTLDETT?RENVMOLFNVLLGDNHGLDID
TLDKDVAHDSRSIQPAMLRDDEILTHPVFNRYYSETEMMRYMHSLERKDLALNQAMIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKRVXKLKNANRFFVASDVHPQTLDVVRTRAETFGFEVIVDDAQKVLDHQDVFGVLLQ
QVGTTGEIHDYTALISELKSRKIVVSVAADIMALVLLTAPGKQGADIVFGSAQRFGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGSCTMKLNAAAEMIPITWPEFAELHPFCPPEQAEGYQQMIAQUADWLVKLTGYDAVC
MQPNSGAQGEYAGLLAIRHYHESRNEGHRDICLIPASAHGTNPASAHMAGMQVVVVAC
DKNGNIDLTDLRAKAEQAGDNLSCIMVTYPSTHGVYEFIIREVCEVVHQFGGQVYLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANMNAQVGITSPGFIGADVSHLNLHKTFCIPHGGGGPGMGPIGVKAHLAPFVPGHSVV
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LPEVGATVSAGDDCAVAESVKAASDIYAPVSGEIVAVNDALSDSPELVNSEPYAGGWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MAQQTPLYEQHTLCGARMVDFHGWMMPLHYGSQIDEHHAVRTDA
GMFDVSHMTIVDLRGSRTREFLRYLLANDVAKLTKSGKALYSGMLNASGGVIDDLIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENPGWYTAYTPYQPEVSQGRLEALLNFQQVTLDLTGLDMASASLLDEATAAAEAMAM
complement(318. .3634)
/note="similar to GenBank Accession Number L20872
(ECGGCVHP): bases 3318 to 3438 differ from the sequence
presented here, as well as from X73958 and D21144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVPKDIQLATPPQVGAPATEYAALAELKAIASRNKRFTSYIGMGYTAVQLPPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GenBank Accession Number D90281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA69071.1"
/db_xref="GI:882433"
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/db_xref="G1:882434"
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                                                                            IGADGANSWLRNKADIPLTFWDYQHHALVATIRTEEPHDAVARQVFHGEGILAFLPLS
DPHLCSIVWSLSPEEAQRWQQASEDEFNRALNIAFDNRLGLCKVESARQVFPLTGRYA
                                                                                                                           RQFASHRLALVGDAAHTIHPLAGQGVNLGFMDAAELIAELKRLHRQGKDIGQYIYLRR
YERSRKHSAALMLAGMQGFRDLFSGTNPAKKLLRDIGLKLADTLPGVKPQLIRQAMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDGRAIALAAGTCQQLARIGVWQSLADCATAITTVHVSDRGHAGFVTLAAEDYQLAAL
GQVVELHNVGQRLFALLRKAAGGVTLHCPDRVANVARTGSHVEVTLESGETLTGRVLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADGTHSALATÄGGVDWQQEPYEQLAVIANVATSVAHEGRAFERFTQHGPLAMLPMSDG
SCSLWWCHPLEREEVLSWSDEKFORELQSAFGWRLGKITHGKRSAYPLALTHARS
ITHRTVLVGNAAQTLHPLAGQGFNLGMRDVWSLTTLTQAQERGEDMGDYGVLCRYQO
RRQSDREATIGVPDSLYHLEANRWAPLVVGRNIGLMTWBLFFPARDVLAQRTLGWVDR
/translation="MQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEQRVQEPLAANA
PPQLRVSAINAASEKLLTRLGVWQDILSRRASCYHGMEVWDKDSFGHISFDDQSMGYS
                                                    HLGHIVENSVIHYALWNKAHQSSDITLLAPAELQQVAWGENETFLTLKDGSMLTARLV
                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MSVIIVGGGMAGATLALAISRLSHGALPVHLIEATAPESHAHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQNSDFWYFTGFNEPBAVLVLIKSDDTHNHSVLFNRVRDLTAEIWFGRRLGQDAAPEK
LGVDRALAFSEINQQLYQLLNGLDVVYHAQGEYAYADVIVNSALEKLRKGSRQNLTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATMIDWRPVVHEMRLFKSPEEIAVLRRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPVNGKFTQAQREIYDIVLESLETSLRLXRPGTSILEVTGEVVRIMVSGLVKLGILKG
DVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYGQDRSRILEPGMYLTVEPGLYIAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MLMSIQNEMPGYNEMNQYLNQQGTGLTPAEMHGLISGMICGGND"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFNRHGARYPSYNTIVGSGENGCILHYTENECEMRDGDLVLIDAGCEYKGYAGDITRT
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RADALAGWVNHFLLGLGVTQPKLDKVTGETGEAIDDLRNIAQLGYDEDEDQEELEMSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSEISRQEFQRRRQALVEQMQPGSAALIFAAPEVTRSADSEYPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MSAQPVDIQIFGRSLRVNCPPDQRDALNQAADDLNQRLQDLKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7749. .9599)
/note="similar to GenBank Accession Number D00398
(ECOAPP2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEVPEQYRGIGIRIEDDIVITETGNENLTASVVKKPEEIEALMVAARKQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF_f441; third start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEIIEYVRVAALLCHDTFTHPQPTAPEVQKPTLH
                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA69075.1"
/db_xref="G1:882437"
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/db_xref="G1:882438"
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/db_xref="GI:882439"
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/db_xref="GI:882440"
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                                                                                                                                                                                                     complement(6731. .7909)
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/note="ORF_0109"
/codon_start=1
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                                                                                                                                                                                                                                                                                                         'note="ORF_f392"
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/gene="ssr"
                                                                                                                                                                                                                                                                                 "gene="ubiH"
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                                                                                                                                                                                                                               /gene="ubiH'
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                                                                 to GenBank Accession Number X01238
                                                                                                                             Length 141744;
                                                                                                                                                                        Indels
                                                                                                                             Score 82.6; DB 2; I
Pred. No. 1.4e-12;
O; Mismatches 234;
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10374. .10556
/gene="ssr"
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/note="similar t
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S. venezuelae pik
S. venezuelae pik
Nucleotide sequenc
Recombinant cosmid
Sequence encoding
Corynebacterium gl
Corynebacterium gl
Human TGF-beta act
Human TGF-beta act
Human TGF-beta act
Polynucleotide seq
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Human BT-beta act
Human BT-cohn
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Human BT-2 antigen
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AAZ87318
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AAX90757
AAX90757
AAX56285
AAX628320
AAA89224
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AAX56289

33,34,48 33,34,48 33,34,48 33,34,50 34,31 34,31 34,31 34,34

Human low adenosin Human adenosine re Corn raffinose syn Human low adenosin

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Corynebacterium q1	DNA encoding Lysg,	BCG deletion regio	Genomic fragment #	Stealth virus nucl	Rice raffinose syn	Sequence of BamHI	P. aeruqinosa tfdA	N. meningitidis pa	Neisseria meningit	S. venezuelae macr
QI	AAF71777	AAT96816	AAT33536	AAF28535	AAX84317	AAD00334	AAN80093	AAQ97857	AAA81464	AAF21609	AAZ87299
DB	22	18	17	22	20	21	6	16	21	21	21
Query Match Length DB	993	2374	15239	45613				2058	~	349980	4689
Query Match	100.0	100.0	14.0	5.2	5.2	4.8	4.2	4.2	4.2	4.2	4.0
Score	873	873	122.6	45.4	45.2	41.6	37	37	36.8	36.8	35
ult No.	-	7	٣	4	S	9	7	80	6	10	11
Result No.		υ		υ	O	ပ	U	υ			O

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99DE-1031457.
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99DE-1031478.
99DE-1031510.
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99DE-1031634.
99DE-1031636.
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99DE-1032126.
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99DE-1032922.
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99DE-1040764.
99DE-1040765.
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P-PSDB; AAB79658.
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PRARA BARARA BAR
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Nucleic acids from Corynebacterium glutamicum encoding metabolic · pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids,
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Haberhauer
Schroeder H, Zelder O,
                                                                                                                                                                                              athway proteins, useful for producing filteroorganisms, including organic acids, and purine and pyrimidine bases
                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 226-228; 1737pp; English.
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.

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Sequence 993 BP; 233 A; 256 C; 268 G; 236 T; 0 other;
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                                                                                                                                                      ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc
                                                                                                                                                                                    acatggtttcctcccgtgttcaacgaggtagcttcttggggttggagcaacgctcacgctg
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               0;
 993;
  Length
                Indels
Score 873; DB 22;
Pred. No. 1.9e-268;
Mismatches 0;
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Similarity 100.0%; 3; Conservative 0
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         Best Local Sin
Matches 873;
  Query Match
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360 595 420 480 475 540 600 355 660 295 720 720 780

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234 GCTCCCATGCTAAAAGCAGGAGAAGTGATCCTCCTCGATGAGATACCCATTGACACACGG
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                                  774 GAAGTCCTTGTGCAAGCAGCGCGGAAAATGGTGTTGCTGCAAGCAGAAACTAAAGCGCAA
                                                                                                                                                                                                                            gtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgcgc
                                                                                                                                                                                                                                                                                                 414 TGGGCTGCGATGCCCGTCTTACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTG
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3382..14071
//note= "BCG delta 1 deletion region"
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WB. This sequence has been created from the information given in table 2
                                                   LySG; LySE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA, isolated from Corynebacterium glutamicum, contains the LysG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcctccttagccctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgag 120
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                encoding LysG, LysE and ORF3 from Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 873; DB 18; 100.0%; Pred. No. 2.9e-268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                               complement (1723..2373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 23 and 26; Page -; 16pp; German
                                                                                                                                          Location/Qualifiers
complement (82..954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KERJ ) FORSCHUNGSZENTRUM JUELICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vrlijc M;
                                                                                                                                                                           /*tag= a
/label= LysG
1016..1726
                                                                                                                                                                                                                              /*tag= b
/label= LysE
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/label= orf3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       95DE-1048222
                                                                                                         Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                  DE19548222-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eggeling L,
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Local S
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                  DNA (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5313 ctacatgicaccecticggitgicagicagegeateaagtegitggageageaggtegge 5372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5553 ttttcggccgtgttcgacg-----gtctcggcgacgtcctgctcgacgttcggatc 5603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5664 accgagcggaacccggtgccgggctgccggtgcacccgctgggtgaaatgcgctaccta 5723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
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                                                                                                                                                                                                                  This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta2. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT33537) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                 The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the presence or absense of deletion junctions (see AAR13538-46), or by detecting the presence or absence or absence of the sequences contained within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgagtgttggtatcgcgccccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tttcctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctgcgcttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gaggaccaggaccattccgcgcgctgctacggggagggtgtggcgatgggcgcggtgacc
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                                                                                                                                     Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caagcagcgggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcgtcgctgaaacgcacgcggatcaccattgcggtaaacgccgattccatggcgacatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17; Length 15239;
                                                                                                                                                                                                                                                                                                                                                                                                   Deletion polypeptides are used as components of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15239 BP; 2878 A; 4791 C; 4729 G; 2841 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 122.6; DB 17;
llarity 49.9%; Pred. No. 1.7e-28;
Conservative 0; Mismatches 409;
                                                                                                                                                                                                                                                                                                                                                                                                           mmunological assays and in vaccines
                                                                                                                                                                                          Example 1; Fig 2; 66pp; English
 96WO-US01938
                           95us-0390878
                                                     (PATH-) PATHOGENESIS CORP.
                                                                              Mahairas GG, Stover CK;
                                                                                                          WPI; 1996-393419/39.
                                                                                                                                                                bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 426; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 the deletion.
15-FEB-1996;
                           17-FEB-1995;
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The present invention relates to a Moraxella catarhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarhalis (Branhamella catarhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic library; bacteria; human upper airway; otitis media; sinusitis;
                                                                                                                                                                                                  5903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5844 cgtaaggcetttcgtcgcgccatcaccagaccgacgcactttgtcccgaccacagagggc
                                                                                                                                                                                                                                                                                                                                                  5904 ttcaccgccgcagcgcgcgcgggctgggatggggcatgttccccgagaagctggcagca
                                                                                                                                                                                                                                                                                                                                                                                                                           cccatgctaaaagcaggagaagtgatcctcctcgatgagatacccattgacacaccgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5964 tetecgettgeegatggategttegtacgggtetgegacatacacetegacgteectete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gogatgecegtettaegetteggteecaaagatgtgetteaagaeegtgaeetggaeggg
                                                              geggetaaagetecgteactggegtggaategtgacgatgggetgcaggacatgttggtg
                                                                                                                                    cg---cgtcgatggtcctgtgggggggggggggggtatccattgtcccgtcggcggaaggt
                                                                                                                                                                                                                                                                               tttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bronchopulmonary; endocarditis; meningitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 180-191; 545pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF28535 standard; DNA; 45613 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-2000; 2000WO-US16649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6084 gcggcggcaagcg 6096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatgcagcaatcg 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic fragment #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-041427/05.
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Length 4915;

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Oryza sativa.
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                                  107;
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                 141
                                  Matches
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                                                                                                                                                               10609 ATGAATACCACAAATCTTGCCACTTTTGTTGCAGTTATGCAGACAGGCAGCATCTCTAGT 10550
                                                                                                                                                                                                                              inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                                                                                                                                                                               61 gectecttagecettteeattteeecteggeggtgagteagegggttaaagetetegag 120
                                                                                                   Gaps
                                                                                                                                1 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 60
                                                               Length 45613;
                                                                                               ;
               Sequence 45613 BP; 13249 A; 9346 C; 9947 G; 13071 T; 0 other;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4915 BP; 967 A; 1521 C; 1591 G; 828 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stealth virus; detection; diagnosis; infection; ss.
                                                               Score 45.4; DB 22;
Pred. No. 0.0012;
); Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 40-42; 95pp; English.
                                                                                                                                                                                                                                                                                              10489 GATGAATTTGGGACGCCGTTGTT 10467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stealth virus nucleic acid clone,
                                                                                                                                                                                                                                                               121 catcacgtgggtcgagtgttggt 143.
                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel strains of stealth virus
                                                                                                                                                                                                                                                                                                                                                                             AAX84317 standard; DNA; 4915
                                                               5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US27744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0001184
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                              82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-405521/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MART/) MARTIN W J.
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stealth virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9934019-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin WJ;
                                                                                                                                                                                                                                                                                                                                                                                                               AAX84317;
                                                               Query Match
Best Local S
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                                                                                              Matches
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The present sequence is a cDNA encoding raffinose synthase from clone r1s72.pk0020.d9 isolated from a rice infected leaf CDNA library 11s72. Raffinose synthase is involved in the blosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                 1461 CACTCTTGCTGCTGTTGCTGACGCAGGATCTCTCGACGGTGCAGCGCATGAACTCCGCAT 1402
                                                                                                                                                                 1401 TACTCCCTCCGCTGTGAGCCAGCGCTCAAGGCTTTGGAGACTCTTCTTGGTCAGGTCGT 1342
                                                                                                                                                                                                                                   Gaps
                                                                  cactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctttccat
                                                                                                                                  ttececeteggeggtgagteagegegttaaagetetegageateaegtggggtegagtgtt
                                                                                                                                                                                                    ggtategegeacceaaceggecaaageaacegaagegggtgaagteettgtgeaageage
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice, raffinose synthase; raffinose saccharide; soybean; clone rls72.pk0020.d9; nutritional; soy protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice raffinose synthase cDNA from clone rls72.pk0020.d9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2842 BP; 520 A; 887 C; 954 G; 481 T; 0 other;
Score 45.2; DB 20;
Pred. No. 0.0005;
); Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag* a
/product= "Raffinose synthase"
                                                                                                                                                                                                                                                                                        201 gcggaaaatggtgttgctgcaagcagaaac 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΕΙ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 215..2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 42-43; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                      AAD00334 standard; cDNA; 2842 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO
                                  ..
5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                 Conservative
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P-PSDB; AAY70977.
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               Similarity
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Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                                         Query Match 4.2
Best Local Similarity 53.9
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Using presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaphammer BJ;
                                                                                                                                                                                                                                                                                                                                                         06-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1994;
11-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9518862-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-1995
                                                                                                                                                                                                                                                                                                                               AAQ97857;
                                                                                                                                                                                                                                                                            RESULT 8
AAQ97857/c
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                                                   565 ttcggtcccaaagatgtgcttcaagaccgtgacctggacgggcgcgctcgatggtcctgtg 624
                                                                       625 gggcgcaggcgcgtatccattgtcccgtcggcggaaggttttggtgaggcaattcgccga 684
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Sequence of BamHI/SalI fragment of the tfdA gene which encodes 2,4-dichlorophenoxyacetic acid (2,4-D) mono-oxygenase.
                                                                                                                                                                685 ggccttggttggggacttcttcccgaaacccaagctgctcccatgctaaaagcaggagaa
                                                                                                                                    922 GCGCGGCGCGCCCCCATTGGCGAGGCTGCGGAGGCCCTGCTTGACGCCGTCGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmids and bacteria contg. gene tfdA for 2,4\text{-}D\text{-}mono:oxygenase} isolated using new Alcaligenes eutrophus transposon mutants
                             ö
Length 2842;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance; halogenated aromatic cpd; enzyme;
 Score 41.6; DB 21;
Pred. No. 0.0054;
               Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
748..1608
/*tag= a
/note= "DNA SQ claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 10; 32pp; German.
                                                                                                                                                                                                                                                                                                  AAN80093/c
ID AAN80093 standard; DNA; 2058 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zenk M;
                                                                                                                                                                                                                      745 gtgatcctcctcgatgagat 764
                                                                                                                                                                                                                                              802 crrcrrcrrerccreregr 783
 4.8%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaligenes eutrophus JMP134
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                            Conservative
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(STRE/) STREBER W R.
(MACQ-) MACQUARIE UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streber W, Timmis KN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1988-071716/11.
P-PSDB; AAP80079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       mono-oxygenase; ss.
            Similarity
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              Local Simi
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 Query Match
            Best Loca
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73 ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
                                                                                                                                   Gaps
                                                                                        530 CAGCTTCGCTATTTCGTTGCTGCCGCGGAGGAGGGCAACGTCGGTGCCGCCGCGCGGCGG 471
                                                          13 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Using presence of tfdA gene to select transgenic plants - imparting resistance to 2,4-di:chloro:phenoxy:acetic acid, esp. sweetgum (Liquidamber) trees contg. this gene and plantations of them
                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plant; tfdA gene; 2,4-dichlorophenoxyacetic acid; 2,4-D; herbicide resistance; sweetgum; Liquidamber styraciflua; hardwood; plantation; crop improvement; selectable marker; pUCW200; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A tfdA gene of P. aeruginosa plasmid pRO101, which encodes the enzymes for 2,4-D degradation, was cloned into Agrobacterium tumefaciens vector pB1121 to form pUCW200. This was used to introduce 2,4-D herbicide-resistance into sweetgum, thereby allowing selection of transgenic plants and reducing the cost of
                              ;
Length 2058;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                              65;
DB 9;
0.14;
                              Mismatches
Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
751..1611
/*tag= a
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0
                                                                                                                                                                                133 cgagtgttggtatcgcgcacc 153
                                                                                                                                                                                                          410 GIGITGITGITCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                 AAQ97857 standard; DNA; 2058
 4.2%;
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94US-0179667
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                       P. aeruginosa tfdA gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
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P-PSDB; AAR79659.
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proteins from Neisseria genomic sequences. AAAB1453 to AAAB2414.

Crepresent specifically claimed Neisseria meningitidis genomic DNA represent specifically claimed Neisseria meningitidis genomic DNA requences; AAAB1260 to AAAB1261 to AAAB1254 to AAB1259 and AAAB1304 to AAAB1321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1252 represent Neisseria meningitidis Menb polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition of the composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of blological probes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                      530 CACCITCGCTATTICGTTCCTCCCCGGAGGGCAACGTCGGTGCCGCCGCCGCGGCGG 471
                                                                                                                                                 73 ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
                                                                                                                                                                    caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes methods of obtaining immunogenic
                                       ;
0
Score 37; DB 16; Length 2058;
Pred. No. 0.14;
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Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
                                       Indels
                                     65;
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 353-383; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V, Galeotti C, Mora M, Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                                  AAA81464 standard; DNA; 102634 BP.
                                     ;
0
                                                                                                                                                                                                                     133 cgagtgttggtatcgcgcacc 153
                                                                                                                                                                                                                                                         410 GTGTTGTTGTTCGAGCGCAGC 390
 4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US23573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0103794
99US-0132068
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-318079/27.
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200022430-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          04 - DEC - 2000
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   Query Match
Best Local 3
                    Best Loca
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particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                           62462 atggatgccgtacaattaaaatcatttgtcgccgtcgcgacgagggcaaccttacccaa 62521
                                                                                                                                                                                                                                                                                                                                                                                                                   62522 geogecaaacgacttttecttteceagectgeogtttetgeceaattaaageeettgaa 62581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V;
Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                gcctccttagccctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections - \,
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                      1 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 60
                                                                                                                                                                   Sequence 102634 BP; 23871 A; 24828 C; 27888 G; 26042 T; 5 other;
                                                                                                                                                                                                                              21; Length 102634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
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Scarlato V,
                                                                                                                                                                                                                                                               72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pizza M, Hickey E, Peterson J, Tettelin H,
Galeotti C, Mora M, Ratti G, Scarselli M, S
Frazer CM, Grandi G;
                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                            Score 36.8; DB Pred. No. 0.99; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62582 gaatatgtcggcacgccgctgttcaggcgcac 62613
                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 catcacgtgggtcgagtgttggtatcgcgcac 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF21609 standard; DNA; 349980 BP
                                                                                                                                                                                                                              4.2%;
                                                                                                                                    other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132068.
99WO-US23573.
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                                                                                                                                                                                                                                                                   80; Conservative
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                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 80; Conserv
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AAF21609
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Desosamine and macrolide biosynthetic gene clusters, useful for, e

synthesis of methymycin and pikromycin

2000-160679/14

P-PSDB; AAY77194

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sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21507 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21589 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent FOR primers which are used in the exemplification of the present invention. The NNB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisserian ucleic anids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as diagnostic reagent for detecting the bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or confins sequences within the NNB genome. The DNA sequences provide further construction to the first confins sequences provide and are asset to the search to identify open reading frames provide further construction to the first confins sequences provide and are asset to the search to identify open readium or computer further constructions to the search of a search to identify open readium or computer further constructions to the search of a search of the search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
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Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 other;

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Db 166174 atggatgccgtacaattaaaatcatttgtcgccgtcgcgcacgagggcaaccttacccaa 166233
                                                                                          1 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 60
    Length 349980;
                                              Indels
  21;
    DB
Score 36.8; DE
Pred. No. 1.8;
0; Mismatches
Query Match 4.2%;
Best Local Similarity 52.6%;
Matches 80; Conservative
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Db 166234 gccgccaaacgacttttcctttcccagcctgccgtttctgcccaaattaaagcccttgaa 166293 ò

Db 166294 gaatatgtcggcacgccgctgttcaggcgcac 166325 121 catcacgtgggtcgagtgttggtatcgcgcac 152 ò

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AAZ87299 standard; DNA; 4689 BP
                05-JUN-2000 (first entry)
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                                                    1..4689
/*tag=
                                                               WO200000620-A2
          AAZ87299;
RESULT 11
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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds. S. venezuelae macrolide biosynthetic gene pikAIII, SEQ ID NO:34. Location/Qualifiers Streptomyces venezuelae ATCC15439

/product= "PikAIII" 99WO-US14398 98US-0105537 (MINU) UNIV MINNESOTA. 25-JUN-1999; 26-JUN-1998; 06-JAN-2000

Liu H, Xue Y, Zhao L;

Sherman DH,

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production of blologically active macrolides. The macrolide blosynthetic production of blologically active macrolides. The macrolide blosynthetic proteins are useful for synthesis of methymycin, pikromycin, of polyketide synthesis may be useful to prepare lantiblotics and polyhydroxyalkanoate (PHA) monemers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monemer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug respiratory pathogens, as well
                                                                                                                                                                                                                                The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixcomycin, neomethymycin, nature modes proteins which synthesise methymycin, and/or macrolide biosynthetic gene clusters are useful for these and/or macrolide biosynthetic gene clusters are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. Sequences AA287295-287302 represent macrolide biosynthetic genes from Streptomyces venezuelae ATCC 15439, which encode proteins
                                                                                                                                                                                      Claim 15; Page 415-417; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY77190-Y77197
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Sequence 4689 BP; 648 A; 1882 C; 1572 G; 587 T; 0 other;

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2811 CCACCGCCCGGACAGGTCCGCCTGGCCGGAGGCCGTCAGCGGCTTCCACTCGACGCGGTA 2752
                                                                                                                     406 gatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaa 465
                                                                                                                                                                          466 cttggaaccatgcgccacttggccattgcaaccccctcattgcgggatgcctacatggtt 525
                                                                                                                                                                                                                                                            526 gatgggaaactagattgggctgcgatgccgtcttacgcttcggtcccaaagatgtgctt
                                                                                                                                                                                                                  2931 CCGGGCGGCGAGGCCTCACGGTCGTCGTCGCCCCGGCTTCCAGTACGTCGACCTCCGC
                                                                                                                                                                                                                                                                                                   caagaccgtgaccgggcgcgtcgatggtcctgtggggcgcaggcgcgtatccatt
Score 35; DB 21; Length 4689;
Pred. No. 0.87;
                                              0; Mismatches 145; Indels
      4.0%;
                          45.78;
                                                Matches 122; Conservative
      Query Match
Best Local Similarity
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2751 ACGCCAGTCGTCGCGCGCGCTGGTGGG 2725 646 gtcccgtcggcggaaggttttggtgag 672 AAZ87318/c ID AAZ87318 standard; DNA; 36778 BP AAZ87318; RESULT 12

05-JUN-2000 (first entry)

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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                                                                                                                                                                                                                                   /product= "Pik gene cluster protein #1 (AAY77200)"
15688..26907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product= "Pik gene cluster protein #4 (AAY77203)"
                                                                                                                                                                                                                                                                                                                                                             /product= "Pik gene cluster protein #2 (AAY77201)"
26991..31679
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pik gene cluster protein #3 (AAY77202)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Pik gene cluster protein #4 (AAY80997)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY77200, AAY77201, AAY77202, AAY77203, AAY80997.
S. venezuelae pik (macrolide biosynthesis) gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao L;
                                                                                                                                                                                                                                 Location/Qualifiers
1742..15583
                                                                                                                                                                                       Streptomyces venezuelae ATCC15439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31782..35822
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                                                                                                                                                                                                                                   Key
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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine blosynthetic gene cluster, a fragment or its biologically action, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or
                                                                                                                                            hypercholesterolaemia; crop protection agent; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao L;
                                                                                                                                                                                                                                                                   Streptomyces venezuelae ATCC15439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                           comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, parbomycin, narbomycin, narbomycin, arabomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine of biologically active macrolides. The macrolide biosynthetic proteins of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pixromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be seful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, encourage of the properse of the prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as chemotherapeutics, immunosuppressants, agents to treat asthma, cretronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, as crop protection agents (e.g., fundicides or insecticides) via expression of polyketides in plants. The present sequence represents the macrolide
                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated and purified nucleic acid segment
Desosamine and macrolide biosynthetic gene clusters, useful for, e .g. synthesis of methymycin and pikromycin ^{\circ}
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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                       29801 CCACCGCCGGACAGGTCCGCCTGGCCGGAGGCCGTCAGCGGCTTCCACTCGACGCGGTA 29742
                                                                                                                                                                                                                      29921 CCGGCCGCCGCGCCTCACGGTCGTCGTCGCCCCGGCTTCCAGTACGTCGACCTCCGC 29862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                                                      gatgttttaggagcggtaacccgtgaagctaatcccgtggcggggatgtgaagtagtagaa 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.
                                                                                                                                                                                            cttggaaccatgcgccacttggccattgcaaccccctcattgcgggatgcctacatggtt
                                                                                                                                                                                                                                                                           caagaccgtgacctggacgggcgtcgatggtcctgtgggggcgaggcgcgtatccatt
                                                                                                                                                                                                                                                gatgggaaactagattgggctgcgatgcccgtctacgcttcggtcccaaagatgtgctt
biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439, as given in figure 31.
                                                                               Length 36778;
                                        Sequence 36778 BP; 4758 A; 14303 C; 12864 G; 4851 T; 2 other;
                                                                                                           0; Mismatches 145; Indels
                                                                               Score 35; DB 21;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                         29741 ACGCCAGTCGTCGCGCGCGCTGGTGGG 29715
                                                                                                                                                                                                                                                                                                                                                              646 gtcccgtcggcggaaggttttggtgag 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA287285 standard; DNA; 37948
                                                                                 4.0%;
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                                                                                                           Matches 122; Conservative
                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ87285;
                                                                                  Query Match
                                                                                               Best Local
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                                                                                                                                       406
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CC biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, nephymycin, necombinate or combination of these compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds nearlymycin, participation of biologically active macrolides. The macrolide biosynthetic proteins of biologically active macrolides. The macrolide biosynthetic proteins of biologically active macrolides. The macrolide biosynthetic proteins of arbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to complicate PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the macrolide constructive biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37948 BP; 4901 A; 14718 C; 13311 G; 5018 T; 0 other;
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McDaniel

Tang L,

Betlach M,

Betlach MC,

Ashley G,

BIOSCIENCES INC.

(KOSA-) KOSAN

98US-0087080. 98US-0100880. 99US-0119139. 99US-0134990 97US-0846247 98US-0073538 98US-0141908

28-MAY-1998; 22-SEP-1998; 08-FEB-1999; 20-MAY-1999; 06-MAY-1998 28-AUG-1998 30-APR-1997

> ; 0 31031 TCCCGCGGCCTTCAGCGCCCCAGCAGCTCGGCTTCTGGCTCCGCTCCCGACGGCGACGAT 30972 30971 CCACCGCCCGGACAGGTCCGCCTGGCCGGAGGCCGTCAGCGGCTTCCACTCGACGCGGTA 30912 31091 CCGGGCGGCGAGGGCCTCACGGTCGTCGTCGCCCCGGCTTCCAGTACGTCGACCTCCGC 31032 31151 GAGGTCGTCGAGGAGCGAGCCACGCCGGTGAAGCCGTCGCCGGTCGTCAGTGCGGTGAG 31092 406 gatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaa 465 466 cttggaaccatgcgccacttggccattgcaaccccttattgcgggatgcctacatggtt 525 Gaps 526 gatgggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgctt 0; DB 21; Length 37948; Score 35; DB 21; Length 37 Pred. No. 2.3; 0; Mismatches 145; Indels 4.0%; Query Match Best Local Similarity 45.79 Matches 122, Conservative g g g à q ð ò

Narbonolide synthase; polyketide synthase gene; narbonolide polyketide; C12-hydroxyalse; pick; desosamine biosynthesis; transferase enzyme; ketolide; beta-glucosidase enzyme; Nucleotide sequence of the insert DNA in cosmid pKOS023-27. AAA75633 standard; DNA; 38506 picromycin biosynthesis; ss (first entry) 22-JAN-2001 antibiotic; desosaminyl AAA75633; RESULT 14 AAA75633,

99US-0320878.

27-MAY-1999;

Streptomyces venezuelae

US6117659-A 12-SEP-2000

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are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity
                                                                                                                                                                                                                                                                                                            New recombinant picK hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention. The specification describes a recombinant DNA compound expressing recombinant polyketide synthase genes in host cells for the production of narbonolide, narbonolide derivatives and polyketides that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27943 CCACCGCCCGGACAGGTCCGCCTGGCCGGAGGCCGTCAGCGGCTTCCACTCGACGCGGTA 27884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28123 GAGGTCGTCGAGGAGCGAGACCACGCCGGTGAAGCCGTCGCCGGTCGTCAGTGCGGTGAG 28064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a compound relative to the unhydroxylated compound. The recombinant host cells are useful as genetic systems that allow rapid engineering the narbonolide polyketide synthase. These would be valuable for creating novel ketolide analogs for pharmaceutical applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is used to produce the recombinant DNA compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 gatgititaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagaa 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28063 CCGGCCGCGAGGCCTCACGGTCGTCCGCCCCGGCTTCCAGTACGTCGACCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 gatgggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgctt
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Columns 15-32; 117pp; English.
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Matches 122; Conservative
                                                                                                                                                                                                                                                                   WPI; 2000-610844/58.
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ID AAZ56001 standard;
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synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS. Polyketides are compounds synthesised from 2-carbon units through a series of condensations and subsequent modifications. Modular PKS are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the recombinant cosmid pKOS023-27 DNA sequence which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY67201, AAY67202, AAY67203, AAY67204, AAY67205, AAY67207,
AAY67208, AAY67211.
                        cosmid pKOS023-27; ketolide;
Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
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36159..37439
                                                                                                                                      synthase subunit 1"
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25133..29821
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29924..33964
                                                                                                                                                                                                                                                                                   'note= "Narbonolide synthase subunit
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7529..38242
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                      Narbonolide polyketide synthase; PKS; cosmid pK
antiblotic production; narbomycin; picromycin;
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                                                                                                                                     /note= "Narbonolide
13830..25049
                                                                                     Location/Qualifiers
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proteins make up the narbonolide PKS (PICAI, PICAII, PICAII and PICAIV). PICAII includes the loading module and extender modules 1 and 2, PICAII includes extender modules 3 and 4, PICAIII includes extender module 5 and recludes extender module 5 and 2. PICAII includes extender module 5 and PICAIV includes extender module 6 and a type II thioesterase domain. The second type II thioesterase domain is found on the PICB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid pKOSO3-27. Narbonolide is cransferase enzyme is required for this conversion, and the desosamine biosynthetic genes are also found in cosmid pKOSO3-27. The recombinant DNA of the invention is used to express, in transformed cells, narbonolide (or its derivatives) or other ketolides (particularly narbonolide (or its derivatives) or other ketolides (particularly hybrids), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human or veterinary
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Scanning the human genome JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) MEDLINE 99380589 COMMENT Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center	University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC Library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)	or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 652 row: A column: 21 Seq primer: SP6 class: BAC ends High quality sequence stop: 436. FEATURES Location/Qualifiers 1. 436 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate=652 Col=21 Row=A" /clone="Plate	/sex="male" //sex="male" //note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" BASE COUNT 91 a 108 c 119 g 116 t 2 others	Query Match 4.7%; Score 40.6; DB 228; Length 436; Best Local Similarity 59.3%; Pred. No. 0.21; Matches 67; Conservative 0; Mismatches 46; Indels 0; Gaps 0; Qy 209 tggtgttgctgcaagcagaactaaagcgcaactatctggacgcttgctgaaatcccgt 268	Oy 269 taaccatcgccatcaacgcagattcgctatccacatggttcctcccgtgttc 321	ACCESSION AL108460 VERSION AL108460.1 GI:5628764 KETWORDS SOURCE fruit fly. SOURCE fruit fly. ORGANISM Plasmid Drosophila melanogaster Enkaryota; Metazaa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazaa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazaa; Budopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. REFERENCE 1 (bases 1 to 1101) AUTHORS Genoscope. AUTHORS Genoscope. AUTHOR Direct Submission JOURNAL Submission JOURNAL Submission JOURNAL SUPPRICE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) - Web: www.genoscope.cns.fr) COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
SUMMARIES Query Match Length DB ID Description	436 228 AQ405681 1101 219 CNS017SY 925 219 CNS0091P 667 149 BF503196 650 149 BF465823 660 238 AQ481405 660 238 AZ135253	4.1 835 32127284 AZ127284 OSJT27284 CSJT27284 CSTT27284 CSTT27284 <td>.0 528 187 R21101 Y R2101 Y</td> <td>449 16 A1123743 A1123743 A1123743 A123743 A123743 A123743 A123743 A123743 A123743 A123743 A123743 A123743 A1237344 ANG 245 A123 A1237344 A</td> <td>.9 563 149 BF500739 .9 566 142 BB575330 .9 556 142 BB575330 .9 622 142 BB578396 .9 622 16 AI109136 .9 623 104 AI47010 .9 628 21 AI513839</td> <td>AQ405681 436 bp DNA GSS 13-MAR-1999 HS_5076_A1_A11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=652 Col=21 Row=A, DNA sequence. AQ405681. AQ405681. GSS. human. Humo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 436) 1 (bases 1 to 436) Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L. Sequence-tagged connectors: A sequence approach to mapping and</td>	.0 528 187 R21101 Y R2101 Y	449 16 A1123743 A1123743 A1123743 A123743 A123743 A123743 A123743 A123743 A123743 A123743 A123743 A123743 A1237344 ANG 245 A123 A1237344 A	.9 563 149 BF500739 .9 566 142 BB575330 .9 556 142 BB575330 .9 622 142 BB578396 .9 622 16 AI109136 .9 623 104 AI47010 .9 628 21 AI513839	AQ405681 436 bp DNA GSS 13-MAR-1999 HS_5076_A1_A11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=652 Col=21 Row=A, DNA sequence. AQ405681. AQ405681. GSS. human. Humo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 436) 1 (bases 1 to 436) Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L. Sequence-tagged connectors: A sequence approach to mapping and
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ORIGIN

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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
PP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                  ö
d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 ttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaacttg
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                                                                                                                                                                                                                                                                                                           Query Match 4.4%; Score 38.8;
Best Local Similarity 14.4%; Pred. No. 0.
                                                                                       1. 1101
/organism="Drosophila me/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN37L08"
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                                                                            Location/Qualifiers
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TITLE
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chawez, C., Chew, M., Dorsett, V., Farfan, Lio, Frise, E., George, R., Gonzalez, M., Guarlin, H., Harris, N., Li, P., Liao, G., Miranda, A., Mirans, S., Mungall, C.J., Nunoo, J., Pacleb, J., Park, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Lewis, S. E., Berkeley, Drosophila Gene Collection Project
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NY. The library is named RPCI-98 and was constructed by partial. BECRI digestion of Drosophila DNA provided by the BGCP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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AT19123. Sprime AT Drosophila melanogaster adult testes POTB7
Drosophila melanogaster CDNA clone AT19123 5 similar to CG17137:
FBBN0017137 last_updated:000321, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 ggagcaacgeteaegetgegettggaagatgaagegeaeaeattateettgetgeggegt 402
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Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 667)
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                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 219;
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ilarity 15.0%; Pred. No. 2.1;
Conservative 130; Mismatches 142;
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Best Local Similarity
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/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Olique-dT priming. Directionally
Cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 171 c 269 g 172 t
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/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
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AF19875.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster CDNA clone AT19875 5 similar to CG13768:
FBan0013768 last_updated:000321, mRNA sequence.
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//lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
//note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoR Site_2: Xho1; The mRNA for the testis library was made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 gggcgcgtcgatggtcctgtggggcgcaggcgcgtatccattgtcccgtcggcggaaggt 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 GGGCGCTTCCTGCTCGGTGGGGGCCCCTGGCGGGTATCCATGTTCCGGTGCTGCTGGT 273
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hit genomic sequence AE003614
blate: AT.198 row: G column: 3
High quality sequence stop: 533.
Location/Qualifiers
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/db_xref="taxon:7227"
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Unpublished (2000)
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Pred. No. 6.2;
0; Mismatches 35;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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                                                                          /clone_lib="NIH_MGC_44"
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AUTHORS
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                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
| Mp_xrei="taxon:7227"
| Aclone="AT19123"
| Aclone=lib="AT Drosophila melanogaster adult testes pOTB7"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 785)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 cgggcgcgtcgatggtcctgtggggcgcaggcgcgtatccattgtcccgtcggcggaagg 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 ttttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgc 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 CGGTGGTGAAGAACTCAATTGGTCAGGGTCTTGCAGTCGATCGCCAGATGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 149; Length 667;
One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 36; DB : 52.7%; Pred. No. 5.9; Live 0; Mismatches
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                                                                                                       hit genomic sequence AE003630
Plate: AT.191 row: B column: 11
High quality sequence stop: 545.
Location/Qualifiers
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Tissue Procurement: ATCC
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Matches 78; Conservative
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Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(heverley@borcim.wustl.edu)
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/clone="LMA_FV1_Im40b11"
/clone="LMA_FV1_Im40b11"
/clone_llb="Le1shmania major FV1 random genomic library"
/lab_host="T00P10 (Invitrogen)"
/note="vector: p2ero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, J., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvill, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA other GSSs: landobil. XI Other GSSs: landobil. XI Contact: Akopyants, NS / Beverley, SM
from testes and seminal vessicles hand dissected from 0-3
                   day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."
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Leishmania major genomic clone LMAJFV1_lm40b11 5', DNA seguence.
                                                                                                                                                                                                                                                                                                                                                                       188 credacaracrecrecargaaraccaaaccaccaccaaccaccaaccara 247
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                     Length 650;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                  DB 149;
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                                                                                                                                                                                                               Score 35.8; DI
Pred. No. 6.8;
                                                                                                                                                                                                            Query Match 4.1%; Score 35.8; D
Best Local Similarity 65.8%; Pred. No. 6.8;
Matches 52; Conservative 0; Mismatches
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Location/Qualifiers
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Class: shotgun
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Fax: 314 286 1810
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this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline Phosphase and ligated into pZero-2 vector's EcoRV site." 97 c 16 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI; three is the most important food crop in the world. Balf of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA GSS 02-JUN-2000
Rice BAC Library (ECORI) Oryza sativa genomic
                                                                                                                                                                                                                                                                                                                        185 GTCCGTAGCGGCAGTGCTGCGAGAACCTCACCTCAAGCAGCGCGCAGTTGCTGGTGCGGGCT 244
                                                                                                                                                                                                                                                                                                                                                                                          245 ACTAGCAGTAATCGCAGCAGCAAACCGGGAGGGATCGTGAAGACCTGGTTAGCCACGGC 304
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                                                                                                                                                                                                                                                                                                                                                                       219 gcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaaccatcgc
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A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                                                                                                                                                                        Length 393;
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/db_xref="taxon:4530"
/clone="0sJRBb0115C04f"
/tlone=lib="cUGI Rice BAC Library (EcoRI)"
/tlssue_type="Leaf"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                        DB 234;
                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: GTAAAACGACGGCCAGTG Class: BAC ends
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Clemson University Genomics Institute
                                                                                                                                                                                      Score 35.6; Di
Pred. No. 6.8;
0; Mismatches
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High quality sequence stop: 590.
Location/Qualifiers
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ilarity 53.6%;
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Oryza sativa
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cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using Ecori as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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/note="Wector: pBACindigo; Site_1: EcoRI; Site_2: EcoRI;

Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
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1 (bases 1 to 835)
Wing, R. A. and Dean, R. A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA GSS 02-JUN-2000
Rice BAC Library (EcoRI) Oryza sativa genomic
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/db_xref="taxon:4530"
/clone="csynub0084706f"
/clone_lib="CuGI Rice BAC Library (EcoRI)"
/tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
                                                                                                                                                                                                                                                                                                                                                                Score 35.6; DB Pred. No. 7.8; 0; Mismatches
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OSJNBb0084J06f CUGI Rice BAC Librar
clone OSJNBb0084J06f, DNA sequence.
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High quality sequence stop: 745.
Location/Qualiflers
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Seq primer: GTAAAACGACGCCAGTG
Class: BAC ends
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AZ127284.1 GI:8202809
                                                                                                                                                                                                                                                                                                                                                                  1 4.18;
Similarity 57.08;
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Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Whole spike"
/dev_stage="Spikes at 5, 10, 15 and 20 days after
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Pred. No. 8.3;
0; Mismatches 49;
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Site_1: ECORI; Site_2: XhoI; Spikes at 5, 10, 15 and 20 days after anthesis were heat stressed under two conditions at Texas Tech University (D. Zhang in HT Nguyrn lab): (1) at 38 C for 4 hours and (2) 5 days of cyclic treatment' of 38 C for 4 hours. Total RNA and poly(A) RNA were prepared, a cNAA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton, Malatrasi) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors). a lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 537)
Qutob, D., Hraber, P.T., Sobral, B.W.S. and Gijzen, M.
Comparative analysis of expressed sequences in Phytophthora sojae 20267956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524
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Phytophthora.
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9-3E-MY PsojaeMY Phytophthora sojae CDNA, mRNA sequence.
BE582886
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1391 Sandford Street, London, Ontario, Canada NSV 4T3
Tel: 519 457 1470
Fax: 519 457 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 TCTTGGTGCCGAGGTGGACGTCGGCGGCGAGCATCATCTGGATGTCCTGCTCG
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/strain="race 2, strain P6497"
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4.1%; Score 35.4; Di
Best Local Similarity 50.3%; Pred. No. 8.8;
Matches 87; Conservative 0; Mismatches
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/clone_lib="PsojaeMY"
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Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Bp 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
using E. coli host strain XL1 Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XLOLR. Sequenced using T3 primer: 5' ATT AAC CCT CAC TAA AGG GA 3'."
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Genoscope.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR28N12"
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu(kazusa.or.jp, URL.http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 424)
1 (bases 1 to 424)
28amizu,E., Murar,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
DNA Res. 7 (5), 305-307 (2000)
20539644
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                          5% to 0.04% CO2 Chlamydomonas 5', mRNA sequence.
                                                                                                                    554 HKCGTGTKSCGCGWGDCGYKYTGRKCWBHMSGAVCKMMGCSBTGYTGYMTCGVGNGSKCG 495
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    424
/organism="Chlamydomonas reinhardtii"

                                          DB 219;
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85; Mismatches
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reinhardtii CDNA clone LCL090h04_r:
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/clone_lto_035aio_r
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/clone_lto_contains reinhardtii 5% to 0.04% CO2".
/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
/hot; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%.
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Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonas reinhardtii
Eukaryota, Viridiplantes, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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                                                                                                                                                                                                                                                                     AV627993 437 bp mRNA EST 15-DEC-2000 AV627993 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LCL035a10_r 5', mRNA sequence.
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Pred. No. 12;
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/db_xref="taxon:3055"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The CDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
169 c 163 g 93 t 1 others
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                                                                                                                                                                                                                                                    Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
The First Laboratory for Plant Gene Research
Tha Isausa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
LocatLon/Qualifiers
1. :529
/organism="Chlamydomonas reinhardtii"
                                  Eukaryota: Viridiplantes: Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 529)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K., Nakamiza,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2 bunk Res. 7 (5), 305-307 (2000)
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/clone="LCL059f01_r"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
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Chlamydomonas reinhardtii
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Search completed: September 14, 2001, 06:59:27 Job time: 12074 sec Appli Appli Appli

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Scoring table:

Searched:

Database

Perfect score:

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Sequence:

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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCE: 18
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
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                      US-09-385-028-15
US-07-867-194-3
US-07-867-194-5
US-08-927-219-50
US-08-927-219-130
US-08-927-219-130
US-08-127-139-130
US-08-127-139-130
US-08-127-133-15
US-08-127-173-15
US-08-131-173-15
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       -037-230D-23
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STREET: One Market Plaza, Steuart Street
STREET: Floor
CITY: San Francisco
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Pred. No. 8.3e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08390878 Patent No. 5700683 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 153
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TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
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49.98;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15239 base pairs TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.9
Matches 426; Conservative
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California
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                                                                                   ; Search time 93.36 Seconds
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/cgnl_7/ptodata/1/ina/5B_COMB.seq:*
/cgnl_7/ptodata/1/ina/6A_COMB.seq:*
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/cgnl_7/ptodata/1/ina/backfilesl.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-205-697A-18
PCT-US95-02576-18
US-08-685-625A-5
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PCT-US95-02576-27
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US-08-142-368A-23
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                                                            OM nucleic - nucleic search, using sw model
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US-08-1
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Maximum DB seq length: 2000000000
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TITLE OF INVENTION: tfdA Gene Selectable Markers in Plants and the TITLE OF INVENTION: Use Thereof NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESS: Sterne, Kessler, Goldstein & Fox
  ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
                    5373 CAGGIGCIGGIGGICAGGGAAAAGCCAIGICGGGCGACGACGCAGGIAICCCGCIGIIG
                                                                                                                                                       193 caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
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                                                                                                                                                                                              gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08358117 Patent No. 5608147 GENERAL INFORMATION:
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COUNTRY:

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MICROORGANISMS AND PLASMIDS FOR 2,4-DICHLOROPHENOXYACETIC ACID (2,4-D) MONOOXYGENASE FORMATION AND PROCESS FOR THE PRODUCTION OF THESE PLASMIDS AND STRAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 CTGCATATTTCCCAGCCCCCGGTCACGCGACAGATTCACGCGCTCGAACAGCATCTGGGC
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1;
Pred. No. 0.073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                               1405.0030001
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APPLICANT: TIMIS, KENNETH N.
APPLICANT: ZENK, MEINHART H.
TITLE OF INVENTION: MICROORGANISMS AN
TITLE OF INVENTION: 2,4-DIGHLOROPHENO
TITLE OF INVENTION: FORMATION AND PRO
TITLE OF INVENTION: RAND STRAINS
                                                                                         .... US/08/358,117 15-DEC-1994
                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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                                                                                                                                           FILING DATE: 15-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESEMOM, ROBERT W.
RECISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1405
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
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                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2560
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2058 base pairs
                                                                                                    CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
751..1611
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CORRESPONDENCE ADDRESS:
                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-358-117-1
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                                                                                   SOFTWARE:
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GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules TITLE OF INVENTION: and Uses Therefor NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                      28123 GAGGTCGTCGAGGAGCGAGACCACGCCGGTGAAGCCGTCGCCGGTCGTCAGTGCGGTGAG 28064
                                                                                                                                      466 cttggaaccatgcgccacttggccattgcaaccccctcattgcgggatgcctacatggtt 525
                                               406 gatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaa 465
    Gaps
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  0; Mismatches 145; Indels
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION YOATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 27883 ACGCCAGTCGTCGCGCGCGTGGTGGG 27857
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08205697A Patent No. 6218510
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Matches 122; Conservative
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Best Local Similarity
Matches 108; Conserva
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STRANDEDNESS:
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US-08-205-697A-27
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APPLICANT SHIEST, Gary
APPLICANT SHIEST, Gary
APPLICANT SHIEST, Malanie C.
APPLICANT BETLACH, Mary C.
APPLICANT WCDANIEL, RODERT
APPLICANT TANG, L1
TITLE OF INVENTION. RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REERRENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-02-08
EARLIER FILING DATE: 1998-05-08
EARLIER FILING DATE: 1998-05-28
EARLIER FILING DATE: 1998-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Indels
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Best Local Similarity 53.9%; Pred. No. 0.073
Matches 76; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09320878A Patent No. 6117659 GENERAL INFORMATION:
                                   ATTORNEY AGENT INFORMATION:
NAME: LAWRENCE, WILLIAM F.
REGISTRATION NUMBER: 28,029
REFRENCE/DOCKET NUMBER: 5144
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0500
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptomyces venezuelae US-09-320-878-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 cgagtgttggtatcgcgcacc 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 GTGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-470-588-1
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07-JUN-1995
4: 800
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                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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Best Local Similarity
FILING DATE: 07
CLASSIFICATION:
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270 GAAAGGAGGAGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02109
                                                                                                                                                                                                                                                                               RESULT 7
US-08-147-772-1/c
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0
                     181 gaagteettgtgeaageagegeggaaaatggtgttgetgeaageagaaactaaagegeaa 240
                                                                                                                241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
                                                                                                                                                                                                        301 acatggtttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctg 360
                                                                                                                                                         270 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 211
                                                                                                                                                                                                                                                    210 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules TITLE OF INVENTION: and Uses Therefor
                                                                 330 GATGGCAGAATGGAAACATGGCAAAAGAAGAGGTTACATTAAGCAAATTGCATATGGGGA
                                                                                                                                                                                                                                                                                                DB 5; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.8%; Score 33; DB 5; Length 379
Best Local Similarity 46.4%; Pred. No. 0.6;
Matches 108; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPPC
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-0595-02576-27/c
; Sequence 27, Application PC/TUS9502576
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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PCT-US95-02576-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300

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301 acatggtttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctg 360
                                                                                              210 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Slasubramanian
APPLICANT: Baskar, Susubramanian
APPLICANT: Baskar, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Teeman, Gordon J.
APPLI
                                                                                                                                                                                                            361 cgcttggaagatgaagcgcacacattatccttgctgcggcgtggagatgtttt 413
                                                                                                                                                                                                                                                                   LOCATION: 318 to 1181 bp IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Open reading frame (translated region)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/08147772
; Patent No. 5858776
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CLONE: B7, Raji clone #13
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFRENCE/CDCKET NUMBER: RPI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT:
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1442 GATGGCAGAATGGAAACATGGCAAAAGAAGAGGTTACATTAAGCAAATTGCATATGGGGA 1383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1322 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gaagtccttgtgcaagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: AAHLVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2; Length 149
Pred. No. 1.1;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                   REGISTRATION NUMBER: 36,207
REPERRENCE/DOCKET VUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE GIRARACTERISTICS:
LENGTH: 1491 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/101,62/
FILING DATE: 26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08101624; Patent No. 5942607; GENERAL INFORMATION:
                   ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 46.4
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         ; TISSUE TYPE: Jymphoid
; CELL TYPE: B cell
; CELL LINE: Raji
US-08-456-104-5
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapien
                                                                                                                                                                                                                                                           nucleic acid
EDNESS: double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-101-624-22/c
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APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: OF STAY S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1442 GATGGCAGAATGGAAACATGGCAAAAGAAGAGGTTACATTAAGCAAATTGCATATGGGGA 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1322 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1382 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 gaagtccttgtgcaagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 acatggtttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctg 360
                                                                                                        AUTHORS: FREEMAN, GORDON J.
AUTHORS: SEGLIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITHAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression on Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
3.8%; Score 33; DB 2; Length 1491;
Best Local Similarity 46.4%; Pred. No. 1.1;
Matches 108; Conservative 0; Mismatches 125; Indels
                   NAME/KEY: Alternate polyadenylation signal LOCATION: 1474 to 1479 bp IDENTIFICATION METHOD: similarity to other pattern PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               1: FROM 1 TO 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/456,104 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08456104 Patent No. 5861310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Pred. No. 1.1;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: Similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B7, A New Member Of The Ig Superfamily With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22: FROM 1 TO 1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
                                                           REFERENCE/DOCKET NUMBER: RPITELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5441
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%;
Best Local Similarity 46.4%;
Matches 108; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UBLICATION INFORMATION:
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JOURNAL:
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AUTHORS:
AUTHORS:
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1382 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 1323
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APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
CLASSIFICATION: 536
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                             GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: GRANT, HUGH
APPLICANT: INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 125;
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Pred. No.
                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-751-767A-5/c
;. Sequence 5, Application US/08751767A
; Patent No. 5994104
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
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TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 46.49
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                             ARLINGTON
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COUNTRY: U
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US-08-751-767A-5
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1322 AGAAGGTGAGGTGAGGTGAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 1263
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Pred. No. 1.1;
0; Mismatches 125; Indels
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APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and TITLE OF INVENTION: 1055 Therefor NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491
US-08-153-262-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTENT AFFLICATION DATE: US/08/479,744A FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 3-NOV-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 3-NOV-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: LAHIVE & COCKFIELD, LLP 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-479-744A-28/c; Sequence 28, Application US/08479744A patent to 6084067; Seturn INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: RP1 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                       46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                             Query Match
Best Local Similarity 46.4
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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STREET: 60
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                                       APPLICANT: NADLER, LEE M.

TITLE OF INVENTION: DNA Encoding B7, A New Member

TITLE OF INVENTION: Of The 1gG Superfamily With Unique Expression On

TITLE OF INVENTION: Activated And Neoplastic B Cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
The Journal of Immunology
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LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
                                                                                                                                                                            E: The Dana-Farber Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION NUMBER: US/US/133,202
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEPHONE: (203) 255-8906
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 Dase pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS/DOS
SOFTWARE: WORDPERFECT 5.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,262
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LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
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FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.
  FREEMAN, GORDON J. FREEDMAN, ARNOLD S.
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CELL TYPE: B cell
CELL LINE: Raji
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: U.S.A.
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                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2714-2722
                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE:
                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
AUTHORS:
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AUTHORS:
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VOLUME: 1
                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE:
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PAGES:
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TITLE: B7, A New Member Of The Ig Superfamily With TITLE: Unique Expression On Activated And Neoplastic B Cells JOURNAL: The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Open reading frame (translated region) LOCATION: 318 to 1181 bp IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Alternate polyadenylation signal LOCATION: 1474 to 1479 bp IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 28: FROM 1 TO 1491
                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEALELING PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 3-NOV-1993
ATORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 35,007
REGISTRATION NUMBER: 36,007
REGISTRATION NUMBER: 36,007
REGISTRATION NUMBER: 36,007
REGISTRATION NUMBER: 36,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: RPI-004CP2 TELECOMMUNICATION INFORMATION:
                                                    ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: CDNA in PCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
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NADLER, LEE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                            CORRESPONDENCE ADDRESS:
                                                                                                                            Massachusetts
                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  NUMBER OF SEQUENCES:
                                                                                                        Boston
                                                                                                                                                                           21P: 02109
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AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFERY M.
LEE, GRACE
WHITWAN, JAMES F.
INDLER, LEE M.
BY, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1262 CCCACGATCCATGTATCCCAGAGGATGACGGAGGCTACCTTCAGATCTTTT 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.8%; Score 33; DB 3; Length 1491;
46.4%; Pred. No. 1.1;
tive 0; Mismatches 125; Indels
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APPLICANT: Freeman, Gordon J.
APPLICANT: Freeman, Gordon J.
APPLICANT: Gray, Gary S.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. G130316el CTLA4/CD28 Ligands and TITLE OF INVENTION: Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Alternate polyadenylation signal LOCATION: 1474 to 1479 bp IDENTIFICATION METHOD: similarity to other pattern PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28: FROM 1 TO 1491
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; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-479-744A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-280-757B-28/c
; Sequence 28, Application US/08280757B
; Patent No. 6130316
                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: CDNA in PCDM8 vector
CLONE: B7 Raji clone #13
POSITION IN GENOME:
                          TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
                                                                                                               ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL TYPE: Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.89
Best Local Similarity 46.49
Matches 108; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL:
VOLUME: 1
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AUTHORS:
TITLE: B7
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AUTHORS:

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APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1382 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%; Score 33; DB 3; Length 1491;
46.4%; Pred. No. 1.1;
tive 0; Mismatches 125; Indels
                                                                                                                                                                                                    NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                 LOCATION: 1474 to 1479 bp IDENTIFICATION METHOD: Similarity to other pattern
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DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491
                                                                                                                                                                                                                                                                                            NAME/KEY: Alternate polyadenylation signal
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                                                                IMMEDIATE SOURCE:
LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.4 Matches 108; Conservative
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                       CELL TYPE: B cell
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STREET: bv
    TISSUE TYPE:
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STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
AUTHORS:
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                                                                                                                                                                                                                                              241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
                                                                                                                                                           181 gaagteettgtgeaageagegeggaaaatggtgttgetgeaageagaaactaaagegeaa 240
                                                                                                                                                                                                                                                                                                                                           acatggtttcctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctg 360
                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Blincher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SUGUENES: 4
CORRESPONDENCE ADDRESS:
                                                                     DB 3; Length 1491;
                                                                   Score 33; DB 3; Length 149
Pred. No. 1.1;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY CACENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JABLE FORTY disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09159135
Patent No. 6149905
                                                                   3.8%;
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LENGTH: 1491 base pairs
                                                                Query Match 3.8'
Best Local Similarity 46.4'
Matches 108; Conservative
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ORIGINAL SOURCE:
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
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APPLICANT: Ostrano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
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US-09-159-135-1/c
US-08-280-757B-28
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                                                                                                                                                                                                                                                                                                                                        301
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REFIERENCE/DOCKET NUMBER: 36,207
REFIERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDN

**RANDRE:
**NAME/KEY: CDS
**1001
**NAME/KEY: CDS
**NAME/KEY: C
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; LOCATION: 318..1181
US-08-205-697A-18
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DB 4; Length 1491;

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Search completed: September 14, 2001, 07:51:47 Job time: 12421 sec

September 14, 2001, 03:41:38 ; Search time 2960.24 Seconds (without alignments) 3715.094 Million cell updates/sec 1 gtgtcatcgggcacggttgg......cagattcgctatccacatgg 711 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 1344157 seqs, 7733874588 residues US-09-105-117I-1_COPY_1016_1726 711 OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

2688314 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmbl:* ٠. Database

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ntg_inv2:* ntg_other:* hum7: hum8: rod:* . 9առվ

em_hum5:*
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em_in:* hum2: em_hum4

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gb_sts3: em_sts:* em_sy:* gb_sts2: gb_sy:* em_ov:* em_ro:* em_pl:* em_un:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_rol:*
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gb_in4:*
gb_pr10:*
em_ba3:*

SUMMARIES

NO.	No. · Score	e Match	Match Length DB ID	DB	ID	Description
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ပ	7		7 23/4	7	CGLYSEG	Ayb4/1 C.giutamicu
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ပ	3 43		822	σ	AX063771	AX063771 Sequence
	4 406		1 993	6	AX063767	AX063767 Sequence
ပ	5 81.		33285	m	SCSF8	AL357613 Streptomy
υ	6 71.8	8 10.1	12070	Н	12070 1 AB011413	AB011413 Streptomy
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X73026 E.coli gene
M62865 E.coli chro
X66836 E.coli chro
AC020850 Mus muscu
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AE004916 Pseudomon
AE00456 Escherich
AP002560 Bscherich
L41665 Synechococc
U65741 Aeromonas s
AE004639 Pseudomon
AE004457 Pseudomon
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AE004780 Pseudomon
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Direct Submission
Submitsed (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
Submitted (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
1, Forschungsentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
Location/Qualifiers
                          Z74025 Mycobacteri
AX030085 Sequence
X14436 Escherichia
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U28377 Escherichia
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Vrljic.M., Sahm, H. and Eggeling, L.
A new type of transporter with a new type of cellular function:
L-lysine export from Corynebacterium glutamicum
Mol. Microbiol. 22 (5), 815-826 (1996)
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1ysE gene: lysG gene: Lysine export regulator protein; Lysine
exporter protein: Lysine governor.
Corynebacterium glutamicum.
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Corynebacterium.
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Db 1059 GCCCCAAAAGCAGCCTGTAATCAAGATTCCATGATCACCATCGTGACCTATGGAAGT 1000 Qy 361 acttaagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaa 420	2 2 493933 N Sequence 2 f A93933 N Sequence 2 f A93933.1 G1 Corynebacter M Corynebacter A Corynebacter Corynebacter Corynebacter N Corynebacter A Corynebacter Orynebacter I (bases 1 VIII,C.M. an PROCESS FOR PATENTY OF PATEN	1. 12374 Corganism="Corynebacterium glutamicum"	Db 1179 GCGATGAACAAAAAGACGTCAGAAATTAAACACACGAGAAGAACCGCAATGAGTCCTTCG 1120

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Length 993;

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Query Match

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ACTIONMYCETALED TOTELH, There. Thereof and phydratase; two-component sensor histidine kinase.

STREPtomyces coelicolor A3(2).
SM Streptomyces coelicolor A3(2).
ACTIONMYCETALES: ACTIONDACTERIDAS.
ACTIONMYCETALES: ACTIONDACTERIDAS.
BACTERIA: Firmicutes; Actinobacteridae;
ACTIONMYCETALES: Streptomycineae; Streptomyces.
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Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (05-JUN-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CEB10 ISA E-mail: barrell/Gsanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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                                                                             Indels
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                            Pred. No. 1.4e-113; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SC5F8 33285 bp DNA Streptomyces coelicolor cosmid 5F8. AL357613
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger, K.J. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 33285)
                                    Similarity 100.
06; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Votes
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7

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PARSVEIABEBAGALVRILTDGMDSAFALVTRIREBGLTLVHPFDDPVVVAGQGTVGLFF
BEDSBLILTBCAPSVSRILTVBHVAELVFVRWGVETEGABAMSRALAAGGPLT
VPLSSVVTTLGAPSVSRILTVBHVAELVTEVLVVPDRRBVRGSLALABHAKVWTEPAAG
CLLPAARRVVERVGDGARIGLVVCGGNATVGDMAVWADRFGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="SC5FB.03c, unknown, len: 225 aa. Similar to several proteins of undefined function including: Deinococcus
                                                                  /translation="MIAITEIEAAAERIAGHVVRTPTVPSPGLSALLGVPVTAKLELL
QRTGSFKARGATAKLLSLTEAERAAGVVAVSGGNHGIAVAVMAAALDVKATVVMPRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYRGNLOFERKGOGVGGMLKRAYTGEGLPLMAVRGOGBAWFANBAQNCFVVEVEPGDB
FTVNGRNVLCFDASLSYRIATVKGSGIAGGGLFNSVFTGQGRLGLVCEGNPLVIPVSQ
OYPVHVDTDAVVGWSAGLATSLHRSQSIGSMLRGGSGBAVQLVLQGEGFVVVRPSEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SC5F8.04c, unknown, len: 434 aa. Similar to Streptomyces coelicolor TR:09x9w9(EMBL:AL096743) putative transport associated protein, SC17.21 (399 aa), fasta scores opt: 426 z-score: 449.2 E(): 1.5e-17 38.3% identity in 209 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSDLVPGGNVPLPGGPVSVRVPGGFDVSALVTDEGGKVGGDADF
YFR NQPEAPCARLENDOTLTVDPARLERGARRYVAVGFEDSGFPLGALESPTVLVTDA
RGRYVARFTPARPGETVLLIFPEYRRGGRWYRALGOGYADGLAGLARDFGSYBYDD
RPPEPARFTPARPGETVLLIFVDSARAAGSPAVRPDPRLRSAARAHAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLSIETRDGVSVHQRVVSAGFAYLTVGEHLVSGPRTPAEFVAYCLRAERTRRTLHDTA
FTHAGWACVTGGPSGDTYWTALWAVPLTPDGLARTTAEVVGLTNRERAGAGLPALAVD
ARLTAAAQAHSADMVTRDFYSHTDPDGGKPWDRAAAAGADRRSVGENIACGQRSPAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aa. Similar to several other putative regulators from Streptomyces coelicolor including:
TR:Q9XAN4 (EMBL:AL079355) SC4C6.06 (893 aa), fasta scores opt: 305 z-score: 318.7 E(): 7.7e-11 26.4% identity in 910 aa overlap and TR:Q92573(EMBL:AL035569) SC8D9.18 (1091 aa), fasta scores opt: 857 z-score: 926.1 E(): 0 36.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKGDLFSSEHMVQPATAPGMTVENSKCIRYAVNGEMLARQGAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SC5F8.05c, possible LuxR-family regulator, len: 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      radiodurans TR:09RWP1 [EMBL:AE001920] conserved hypothetical protein (254 aa), fasta scores opt: 467 z-score: 555.6 E(): 1.8e-23 36.6% identity in 205 aa overlap and Streptomyces coellicolor TR:CAB70638 (EMBL:AL137242) SCBF4.12C (239 aa), fasta scores opt: 397 z-score: 474.2 E(): 6.1e-19 36.1% identity in 183 aa overlap."
                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry PF00291 S_T_dehydratase, Pyridoxal-phosphate dependent enzyme, score 210.10, E-value 3.3e-59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dehydratases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein SC5F8.03c."
/protein_id="CAB93731.1"
/db_xref="G1:8347026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/product="hypothetical protein SC5F8.04c."
/protein_id="CAB93732.1"
/db_xref="G1:8347027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1287. .1328)
/gene="SC5F8.02c"
/note="PS00165 Serine/threonine dehydripyridoxal-phosphate attachment site"
complement(1477. .2154)
/gene="SC5F8.03c"
/gene="SC5F8.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC5F8.04c"
complement(2166. 3470)
/gene="SC5F8.04c"
/note="SC5F8.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC5F8.05c"
/note="scfF8.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3562. .6528)
/gene="SC5F8.05c"
complement(3562. .6528)
                                                                                                                                                                                                                                                                                    complement(546. .1412)
/gene="SC5F8.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Juny-vyl-DinyIrameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. If may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 5FB lies on genomic restriction fragment Asel-A bordered by cosmids 5H1 and 4G10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement(492. 1451)

Complement(492. 1451)

Complement(492. 1451)

Complement(492. 1451)

Anote="SC5FB.02c"

Anote="SC5FB.02c"

STATE Complement of the confine dehydratase, len: 319

aa. Similar to many including: Escherichia coli

SW.THOZ_ECOLI(EWBL:M31312) threonine dehydratase catabolic

(EC 4.2.1.16) TdcB (3129 aa), fasta scores opt: 609

Z-Score: 676.6 E(): 3.2e-30 39.4% identity in 312 aa

overlap. Contains a Prosite hit to Serine/threonine
                                                                                                                             are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for

EDS which show significant similarity to other CDS in the database.

The position of possible ribosome binding site sequences are given
where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons

using a specially developed Hidden Markov Model (Krogh et al.,

Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot

program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SC5F8.01c, possible serine/threonine protein kinase, partials CDS, len:> 114 aa. Similar to many proposed Streptomyces coelicolor serine/threonine protein kinases e.g. TR:CAB82014(EMBL:AL161755) SCD63.07 (717 aa), fasta scores opt: 172 z-score: 222.0 E(): 6.8e-05 33.0% identity in 103 aa overlap. Overlaps and extends into CDS SC5H1.01 on the adjoining cosmid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MGRAHVSTHELVAGRYRLFEVVQRETNRVCWSGEDATTGRPCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRIELPEGRAGEAARRAPGRVIRTGETMASLCPGRIAPVLDAVVADGMLWTVTEWVAG
CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                       The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydratases pyridoxal-phosphate attachment site and a Pfam match to entry PF00291 S_T_dehydratase, Pyridoxal-phosphate dependent enzyme."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="nominal overlap with cosmid SC5H1 between bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="putative serine/threonine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative threonine dehydratase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB93729.1"
/db_xref="GI:8347024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SC5F8.01c"
/note="screm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1. .344)
/gene="SC5F8.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1. .108)
/gene="SC5F8.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="cosmid 5F8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nttp://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPLGDLLDRRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 33285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .108.
                                                                      strand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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FEATURES

CDS

CDS

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TDDRRRMDAEYDEMRRRASVAASLVYYEDDRIRSAGPAEHRSLVLSIVIGAGALTALA
ALTGHYLSGRSCGPAMEALEQQERLLADAAHELRTPVAVMRGSVEVAAGAPGGLEGOL
PRRRAADRADDVVENLLTRGRLEAGRTSYGRSRLRLDQLVEEVCAELPEGGPGLESR
LEESVVEADAALVRVAVRNLLDNAVRHGPGSRGAAGRGRTAGDRVRTGVRVADRGPAV
APARLPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="Matqalgtalricyfdrigtgelraealagslgthpratirler
Alaglollsbepgarttaagnviaadapgtwamarattdpvmlkgwblldbsvrt
gettfolyfgtdffgelrehellsarneamsggtritaetvphhydfgrfgrlvdig
ggdgtllasilrahgergvleptaeglagapregglgtriaergldfraapag
gdlyllnsTihdwddavrghirhirdyipdhgsllivepvlpatvpadrpdnvylsd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GREQHCAEGNTOTYNALDRNGEPTYGGYSTHLVVTEKFALSIPEGIALDEAAPLLCAG
ITTYSPLRRWGAGPGKKVAVVGLGGLGHMAVKIAHALGAEVTVLSQSLRKKDDGLKLG
ADHYYATGDPRTFEELAGTFDVILSTVSAPLDFGAYLALLRTEGTLVNVGAPEEPVSL
NLFSLILGNSIAGSAIGGIEETQEMLDFCAVHGLGAEIEVIGAGQVNEAYERVLASD
                                                                                                                                                                                                                                                                                                                                                                          /translation="mrvlLvedDdDlrDvIgaGLrDGGFAWDCASDWPEADVLLHLSA
PCVVLDRWPGSDTLAPLEGRRRAGNSVPVLCTALDSDEBRIAGLESSADDVLAKP
FSWRELVLRVRGESRASARLPSFLGCADVWMDVARHEVRRGGVLLSLSPKBYAVLQD
LLVHRDTVVTRTGLLEHCWDEMADPVSNVVDAVVGLRRKLGSPGLVHTVRGQGFLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="orfs"
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RTGRVLLMRTRPVRFPSGEVALARQLARLEHEAQAALGMSGPGEPTLLPIAVNSDS
LATWSWQPCGACRRSWDSATTAPGGPGPYGRPAAGGAGDGRGDLVAGGGDGLFGPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMRYLPVASPGFADRWLGRRDGTALRELIGEAPVVCFDRRDDLQDAFVRRLGPGARPS
ARRHLVPTSEGFANAVASGMGWVPEVQAEPLLSDGRLVRLAPEPTVDVPLYWQQWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/transl_table=11
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/protein_id="BAA32134.1"
/translation="MARAENPUPPOGIEMVHRTRPEDAFPRNWYRLGRDRFAVEAVLPHDPFFAPVGDDLHDPLLVAEAMRQAAMLAFHAGYGIPLGYHFLLTELDYVCHPEHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGGEPTEIGLEVFCSDLKWRAGLPÅGGRVGWAVHRGDRLAATGVAATRFSTPKAYRRM
RGDVPVEGISLPETAPVPASPAGRARVEDVVLSGTGREGVWELRVDTRHPTLFQRPND
HVPGMLLLEAARQAACLVAGPAGIVPVEARTRFHRYSEFGSPCWIGAVVQPGADEDTV
                                 /translation="VAAPVPAAPHPGPEAAAPAAARLTAAYTLITVVGLACLSWLVIR
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                                                                                                                                                                                                                    /function="two-component regulator protein
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/function="alcohol dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4333. .>5250)
/function="methyltransferase"
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10558. .11598
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/protein_id="BAA32135.1"
/db_xref="G1:3401952"
                                                                                                                                                                                                                                                                                               /product="Orf3"
/protein_id="BAA32131.1"
/db_xref="G1:3401948"
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/protein_id="BAA32132.1"
/db_xref="G1:3401949"
                                                                                                                                                                                     complement(3523. .>4197)
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ORIGIN
identity in 1077 aa overlap. Contains a Prosite hit to PSO0017 ATP/GTP-binding site motif A (P-loop) Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-FEB-1998) to the DDBJ/EMBL/GenBank databases. Takashi Umeyama, University of Tokyo, Department of Agriculture and Life Sciences; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113, Japan (E-mail:aa67103@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-3812-2111)
                                                                                                                                                                                                                                                                                                                     DLLRPLLGRGVLQRPAGGAPGHRLALPASYRADDLHRRHPLRPLLAELVRLPGVERLE
LRPLPDSDVARLVRLLRERRLPDSTVRI VERAEGNAFYAEELVAATDAPAGGVPSGL
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                                                                                                                                                                                                                                                                      GVGKTRTLHEAAGRAAAAGTTVLTGHCVDLGDVGLPYLPFTEILGVLAADERFAAVLA
                                                                                                                                                                                                                                                                                               GHPVADRLLGGGPDDGTDAAPSRLRLFEGVAALLTELADVAPLLLVLEDLHWADQSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.
AB011413.1 GI:3401946
Orf8. Afra. Cf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orf8; AfsA; Orf5; Orf4; Orf3; Orf2.
Streptomyces griseus DNA.
Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces 1 (bases 1 to 12070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18032 CTGCACGTGACGCCGTCCGCGGTCAGCCAGCGGGTGAAGGCACTGGAGCACCGCACCGGC 17973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17972 CGGGTGCTGCTGCTGCGCACCAAGCCGGTGCGGGCGACCGATTCCGGCGCGTGCTGGTG 17913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81.2; DB 3; Length 3
Pred. No. 2.1e-13;
0; Mismatches 93; Indels
                                                                                                                                                               /product-"putative LuxR-family regulator.
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Unpublished (1998)

    12070
/organism="Streptomyces griseus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                        /protein_id="CAB93733.1"
/db_xref="GI:8347028"
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/protein_id="BAA32130.1"
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complement(2660. .3511)
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59.68;
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Mycobacterium boyis deletion region 2, immunogenic protein (mpt64)
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Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.
Molecular analysis of genetic differences between Mycobacterium
J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                                     6283
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                                                                                                       6582 CGCGTCGGACAGGCCCAGATCCCGACCACGCGAGAACGCCGTCGCGGCGGACGCCCTG 6523
                                                                                                                                                                                                                                                                                                                            5462 ACCGGCGGCTGCTGTGGTCAGGGCGTTCGTCATGCGGCGACGCTACGGAGCAGGAACCCC 6403
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1 (bases 10567 to 11392)
Oettinger, T. and Andersen, A.B.
Cloning and B-cell-epitope mapping of MPT64 from Mycobacterium tuberculosis H37Rv
                                                                                                                                  cacgatcggcgcgcattggacaaaagatcaacgcccaaggtgccggcgatgaacaaaaa 194
                                                                                                                                                                                        195 gacgicagaaattaaacacacgagaagaacgcaatgagiccitcgcgcttaaticciig 254
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                                                   19;
                       Length 12070;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                   Indels
                       Score 71.8; DB 1;
Pred. No. 1.3e-10;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insect. Immun. 62 (5), 2058-2064 (1994) 94222581
                                                                                                                                                                                                                                                                                                                                                       375 attggttcttaacatggtttaatatagcttca-----
                        10.18;
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U34849
U34849.1 GI:1049224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium bovis.
                                   Similarity 47.7
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/organism="Mycobacterium bovis"
/db_xref="taxon:1765"
2864. .2888
/show of two imperfect direct repeats located at or near the deletion breakpoints"
/note="this interval is completely absent in the closely related, but avirulent strain Mycobacterium bovis BCG"
10705. .11391
/gene="mpt64"
10705. .11391
/gene="mpt64"
/coce="mpt64"
/coce="mpt64"
/coce="mpt64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRIKIFMLYTAVVLLCCSGVATAAPKTYCEELKGTDTGOACQIO
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IVQGELESKOTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFRNBGELLPEAAGFPQVLV
PRSAIDSMLA"
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Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Direct Submission Submitted (24-Angl-1995) Mark J. Hickey, Molecular Micro., PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA Location/Qualifiers
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/note="one of two imperfect direct repeats located near the deletion breakpoints"

4682 c 4603 g 2759 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4979 CAGGIGCIGGIGGICAGGGAAAAGCCAIGICGGCGACGACGACGCAGGIAICCCGCIGIIG
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Pred. No. 6e-08;
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Stover, C. Kendall and Mahairas, G.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC44034.1"
/db_xref="GI:1049225"
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Sequence 17 from patent
186263
186263.1 GI:3205981
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Best Local Similarity 55.3%;
Matches 166; Conservative
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/db_xref="taxon:155864"
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Virulence-attenuating genetic deletions deleted from mycobacterium
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Perna, N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D., Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A., Posfai,G., Hackett,J., Klink,S., Boutin,A., Boutin,A., Miller,L., Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K., Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C., Welch,R.A. and Blattner,F.R.
Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
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Escherichia coli 0157:H7 EDL933
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                  418 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc
                                                                                                                                                                                                                                                                                                                            5253 CAGCTGGCGCATTGGCTGCCGTGGTCGAACTGGGCAGCTTCGATGCGGCGCGGGAGCGC
                                                                                                                                                                                                                                                                                                                                                                       478 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
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                                                                                                                                                                                                        Length 15239;
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/strain="EDL933"
/serotype="0157:H7"
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                      8.9%; Score 63.2; DB 10;
55.3%; Pred. No. 6.1e-08;
tive 0; Mismatches 128;
                     BCG
Patent: US 5700683-A 17 23-DEC-1997;
                                                           Location/Qualifiers
1. .15239
                                                                                            /organism="unknown"
4791 c 4729 g
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Escherichia coli 0157:H7
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AE005522.1 GI:12517448
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Best Local Similarity 55.3
Matches 166; Conservative
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AUTHORS
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AE005522
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                                                             FEATURES
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/function="phenotype; Not classified"
/note="Residues 1 to 331 of 331 are 99.69 pct identical to
residues 1 to 331 of 331 from Escherichia coli K-12 Strain
MG1655: B2918"
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ETEYARMYDCFISLQIAGGDDLQOIRKGLMEYADLLVINKDODDNHTWYAIARHMYE
SALHILRRKYDEWQPRYCSALEKRGIDETWHAIIDFKTALTASGRLQQVRQQSVE
SALHILRRKYDEWGLGYRYRQTLLAVKNNTLSPRTGLRQLSEFIQTOYFD"
                                                                                                                                                                                                                                                              to 714 of 714 are 99.15 pct identical to of 714 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSNEQEWQQLANKELSRREKTVDSLVQQTAEGIAIKPLYTEADL
DNLEVTGTLPGLPPYVRGPRATMYTAQPWTIRQYAGFSTAKESNAFYRRNLAAGGKGL
SVAFDLATHRGYDSDNPRVAGDVGKTGVAIDTVEDMKVLFDQIPLDKMSVSWTMNGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPVLAFY I I AAEEQGVTPDKLTGT I QND I LKEYLCRNTY I Y PPKPSMR I I AD I I AWCS
GNMPRFNT I SISGYHMGEAGANCVQQVAFTLADGI EY I KAA I SAGLKI DDFAPRLSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGIGMDLFMNVAMLRAARY LWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV ITTIERALAATLGGTQSLHTHRFDEALGLPTDFSRRINRTDJIIQEBESLCRFUDPL AGSYY IESLTDQIYGQARAITQDDBAGGMARAIEAGLFBRMIEBASREQSLIDQGR RVIVGVNKYKLDHEDETDVLEIDNWWYRNEQIASLERIRATRDDAAVTAALNALHAA
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FDAIVAQTEQFLADNGRRPRILIAKMGLDGHDRGAKVIASAYSDLGFDVDLSPMFSTP
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/protein_id="AAG58045.1"
/db.ref="G1571451"
/tb.renslation="MNLSRRNILIKGIFMSYQYVNVVTINKVAVIEFNYGRKLNALSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIHELPSGGRDPLSYDDPLRQI
TRMIQKFPKPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSMTPVNLGVPYNLVGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MINEATLAESIRRLRQGEHATLAQAMTLVESRHPRHQALSTQLL
DAIMPYCGNTLRLGVTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
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AIAVIKEELRVLGEAHTMNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH"
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/note="Residues 1 to 275 of 275 are 100.00 pct identical.
to residues 1 to 275 of 275 from Escherichia coli K-12
Strain MG1655: B2919"
                                                                                                                                                                                            /function="enzyme; Degradation of small molecules: Fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="putative nucleotide-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="methylmalonyl-CoA mutase (MCM)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQERCVAAIYGPGTPMLDSVRDVLNLISQHHD"
2270. 3265
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/note="enterohemorrhagic"
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residues 1 to 714
MG1655: B2917"
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2270. .3265
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/note="Z4254"
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/gene="ygfH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="24257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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gene

CDS

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/protein_i6="AAG$8050.1"
/db_xref="G1:12517456"
/db_xref="G1:12517456"
Aftanslation="MEDLNVUDSTGSWLVANQALLLSYAVNIVAALAIIIVGLII
ARMISNAVNRIMJSRXIDAYVADSTGALVAVGA
AGLAVGLALQGSLSNLAAAGVLLVWFRPPRAGEYVDLGGGVAGTVLSVQIFSTTMRTADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (sites)
Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
                                                                                                                                                              /function="putative transport, Not classified"
/note="Residues 1 to 286 of 286 are 100.00 pct identical
to residues 1 to 286 of 286 from Escherichia coli K-12
Strain MG1655: B2924"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comparative analysis of the whole set of rRNA operons between an enterchemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7922 ccaaaaarccccccccaarcagaccaaarcgcrgaragcgcaaagraaggcaarcara 7981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kimura,S.,
De,H., Iida,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 tecacettgtttgtcatggcgtetttcgetgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2001
FGLAILAAWLAPRLRTAKSQRIINLVVGCVMWFIALQLARDGIAHAQALFS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP002563 266658 bp DNA BCT 07-MAR-2001
Escherichia coli 0157:H7 DNA, complete genome, section 14/20.
AP002563 BA000007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (sites)
Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 atgccaccccagcgcataatatcgagcacgatcggcggcgtcgttggacaaagatcaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 atgagtccttcgcgcttaattccttgtttaatcaccagtacattctgcggtccgatggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7982 ATGTGGTACTGACGACGAATGCCCTGATTCATCACAAAAGCATTTTGTGGGCCGAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%; Score 62; DB 1; Length 10701;
11.4%; Pred. No. 1.3e-07;
ve 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                   /product="putative transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8042 AGAATCAFAGCTGCCCCAAGAGCAAGACCTTGAAAGTA 8079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 agtaaaagactggcccccaaaagcagacctgtaatgaa 326
                          complement(8230; .9090)
                                                                                                             . 9090)
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                                                                                                          complement(8230.
/gene="yggB"
                                                                                                                                                                                                                                                                                                      /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.4%;
                                                         /gene="yggB
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MEDLINE
                               gene
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LOCUS
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KEYWORDS
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                       /function-"putative enzyme; Not classified" hote-Residues 1 to 492 of 492 are 99.39 pct identical to residues 1 to 492 of 492 from Escherichia coli K-12 Strain MG1655: B2920"
                                                                                                                                                                                                                                                                                                                                                    LNHYHDPRVAELADIVIPGAPPRRINSVSIFHAMDRVGTRYQIDERKIYAVVETULARANIN LANHYHDPRVAELADIVIPGAPPRRINSVSIFHAMDRVGTRYQIDERKIYAVVETULARANIN LASHNALDKQNPMCQQIADNVVTFLLQEMAHGRIPPEFLPLQSGVGNINNAVMARLGENPEIPPPMWYSEVLQESVVHLLGETGKISGASASSITISADSLRKIYDNMYFASRIVYRPQEINNPEIIRLGVIALUVGLFFDISGASASSITISADSLRKIYDNMYFASRIVYRPROFINFRUVALVELYRANYTHYGAVDLANGIGGSGDFERNAYLSIFMARBIARGKKISTVPMCSHVDHNBHSVKVITITEQGIADLAGLSPLQRARTIIDNCAHPMYRDYLHRULSTAGSMLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="putative regulator; Not classified"
/note="Residues 1 to 192 of 192 are 99.47 pct identical to
residues 6 to 197 of 303 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDIFISKKMRNFILLAQTNNIARAAEKIHMTASPFGKSIAALEE
OGYTHETRKNNISHKRAOQELYQKLEPVYQRLSALDNEIHNGGRRGREIVIGIDNT
YPTIFDQLISLGORYEGYTAQPVEFSENGYLDNLFDRQLDFIISPQHVSARVQELEN
LTISELPPLRINFLVSRRYEBRQEQELLQELP"
                                                                                                                                                                                                                                                                                                   ANEQHEAKKPYQIRLLTGASISAAADDVLSDADAVSWRAPYQTSSGLKKKINQGAVSF
VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWLTSGIGNAPTWLLRAKKVIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG58048.1"
/db_xref="GI:12517454"
/translation="MKFKVIALAALMGISGWAAQANELPDGPHIVTSGTASVDAVPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATLAIEVNVAAKDAATAKKQADERVAQYISFLELNQIAKKDISSANLRTQPDYDYQDG
KSIIKGYRAVRTVEVTLRQLDKLNSLLLDGALKAGLNEIRSVSLGVAQPDAYKDKARKA
AIDNAIHQAQELANGFHRKLGPVYSVRYHVSNYQPSPMVRMKADAAPVSAQETYEQA
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//function="nesidues 1 to 211 of 211 are 98.10 pct identical to
residues 1 to 211 of 211 from Escherichia coli K-12 Strain
MG1655: B2923"
                                                                                                                                                                                                                                                                         /translation="METQWTRMTADEAAEIIQHNDMVAFSGFTPAGSPKALPTAIARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MFSYYFQGLALGAAMILPLGPQNAFVMNQGIRRQYHIMIALLCA
ISDLVLICAGIFGGSALLMQSPWLLALVTWGGVVFLLWYGFGAFKTAMSSNIELASAE
VLKQGRWKIIATMLAVTWLNPHYYLDTFVVLGSLGGQLDVXPKRWFALGTISASFLWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="phenotype, Not classified"
/note="Residues 1 to 246 of 246 are 100.00 pct identical
to residues 1 to 246 of 246 from Escherichia coli K-12
Strain MG1655: B2922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/product="partial putative transcriptional regulator
                                                                                                                                                   /transl_table=11
/product="putative coenzyme A transferase"
/protein_id="AAG58046.1"
/db_xrefe="G1:12517452"
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/protein_id="AAG58049:1"
/db_xref="G1:12517455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIQFDDQVDVVFQLEPVDQQPAKTPAAQ" complement(7456. .8091)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative actin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG58047.1"
/db_xref="G1:12517453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5878. .6456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6623. .7363)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="24258"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="24258"
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COMMENT

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IIAAEPPNPLVNELIMPDIEKRLEAFVRIAHGIIFPGGVGTAEELLYLIGILMNPA
NYDQVLELILGGPKESADYFRVLDEFVVHTLGENARRHYRIIDDAEEVARGMKKSMP
LVKENRRDTGDAYSFWARTAPDLQMPFEPSHENMANLKLYPDQPVEVLAADLRRAF
SGIVAGNVKEVGIRAIEEFGPYKINGDKEIMRRMDDLLQGFVAQHRWKLPGSAYIPCY
EICT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence-not_experimental
/product="syd protein"
/protein_id="hab37076.1"
/db_xref="G1:13363125"
/db_xref="G1:13363125"
/translation="MDDLTAQALKDFTARYCDAWHEEHKSWPLSEELYGVPSPCIIST
TEDAYWQPOPFTGEONNAV PERAFDIVIOPTIHTFYTTQFAGDMHAQFGDIKLTLLG
TWSEDDFRRYQENLIGHLVTQKRLKLPPTLFIATLEEELEVISVCNLSGEVCKETLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SYD_ECOL1 gi|1789157 percent identity 98 in 181 aa (Conserved in E.coli K-12)" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /traislation="MSSYANHOALAGLTLGKSTDYRDTYDASLLQGVPRSLNRDPLGL
KADNLPFQGTDIWTLYELSWLNAKGLPQVAVGHVELDYTSVNLIESKSFKLYLNSFNQ
FRENWWDEVRQTLERDLSTACAGEVSVALYRLDELEGQPIGHFWGTCIDDQDITIDNY
FEFTDYLENATSGEKVVEETLYSHLKSNCLITHQPWGSIOLQYRGRQIDREKLLRY
LVSFRHHNEFHEQCVERIFNDLLRFCQPEKLSVYARYTRRGGLDINPWRSNSDFVPST
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ENEYLYARRVGNQLGLRELNICTGCGPGAMEAPMKGAAVGHAQORYKDSRFIGMTEPS
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meplewlowvliprmhdllnnnoplegafavapyyemalatdhporalilaeleklda
                                        /note="similar to B2792_ECOLI gil1789156 percent identity 98 in 109 aa (Conserved in E.coli K-12)"
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in 454 aa (Conserved in E.coli K-12)"
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                                                                                                                                                          /evidence=not_experimental
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/product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                              /gene="csrB"
/note="inhibitor of CsrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="csrB"
complement(2444. .2989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ECs3653"
complement(2444. .2989)
/gene="ECs3653"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="CsrB RNA"
                                                                                                            /codon_start=1
/transl_table=11
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/transl_table=11
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4017. .5381
/gene="ECs3655"
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3057. 300F
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/gene="ECs3654"
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                                                                                                                                                                                                  Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli O157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAEDGFVGTWYGNSLLVAEEAEAILTAQGHKATVFEDPELSDW
LPYQDKYVLVVTSTTGGGDLPDSIVPLFQGIKDSLGFQPNLRYGVIALGDSSYVNFCN
GGKQPPALLQPQSAQRYGEMLIDASENPEPETESNFWVEQWGTLLS"
complement(711 1493)
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VLBELDKITADRFAREDKGROPAVTHYRGLATVEMPVATGRYPTRYGLVELEERTGR
KHOLRRHLAHLRHPITGDSKHGDLRQNRSGABHFGILQRLMLHASQLSLTHPFTGEPLT
IHAGLDDTWMOALSQFGWRGLLPENERVEFSAPSGQDGERSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-707-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Sulta, Osaka 565-0871, Japan (E-mail:kenégen-info.osaka-u.ac.jp, URL.http://www.gen.info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
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/note="similar to YQCB_ECOLI gi|1789155 percent identity
99 in 260 aa (Conserved in E.coli K-12)"
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                                                                                                 Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                           Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Ilda,T. Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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1. .266658
/organism="Escherichia coli 0157:H7"
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
20557356
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complement(244. .693)
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complement(1493. .1822)
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
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msdpayninislpsyypdgkslenyiaqtrdkflsaatsstpreapyelnitsatyqs
aipprgtqavvlkvyqnaggthptttykafdmbqayrkpitydtlmqadtdplpvyfp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct
                                                                                                                                                                                                                                                                                                                                                                                                                  Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France B-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rv1981c, (MTCX39.38), ribonucleotide reductase small subunit, len: 322, highly similar to RIR4_SALTY P17424, ribonucleoside-diphosphate reductase (319 aa) FASTA scores, opt: 1402, z-score: 1716.0, E(): 0, (66.0% identity in 315 aa overlap); Also similar to Rv3048c, (MTV012.63c); containsPS00368 Ribonucleotide
   Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
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   Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. ar
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 27, 1998 this sequence version replaced gi:1403436
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complement(968. .1936)
                                                                                                                                                                     Erratum:[[published erratum appears in Nature 1998 Nov
12;396(6707):190]]
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                                                                                       complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
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/gene="mpt64"
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/product="mpt64"
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                                                                                                                                                                                                                                                                   Parkhill, J.
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                                                                                                                                                                                 REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 161484 ATGTGGTACTGACGACGAATGCCCTGATTCATCAAAAGCATTTTTTGTGGGCCGAGCGGC 161543 · · ·
                                                                                                                                                                                                                                                                                                                                                                                   AGVGGMIPLIIMAILAFPMTFFAHRGITRFVLSGKNPGEDITEVVEEHFGIGAGKLIT
LLYFFAIYPILLVYSVAITNTVESFMSHQLGMTPPPRAILSLILIVGMMTIVRFGEQM
IVRAMSILVFPFVGVLMLLALYLIPQMNGAALETLSLDTASATGNGLMMTLWLAIPVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLAAAKEQNISILSYLANHFNAPVIAWAPIIAIIAITKSFLGHYLGAREGFNGWVIK
SLRGKGKSIEINKLNRITALFMLVTTWIVATLNPSILGMIETLGGPIIAMILFLMPMY
AIQKVPAMRKYSGHISNVFVVVWGLIAISAIFYSLFS"
                                                                                                                                                                                                                                                                                                                                                          /translation="METTQTSTIASKDSRSAWRKTDTMWMLGLYGTAIGAGVLFLPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFSFNHSPIISSFAVAKREEYGDMAEQKCSKILAFAHIMMVLTVMFFVFSCVLSLTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinopacetales;
Actinomycetales; Corynebacteriumes; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3850)
Cole.S.T. Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas.S., Barry III,C.E.,
Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.
Tekaia,F., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
                                                                                                          Anote-"similar to SDAC ECOLI gill789160 percent identity 100 in 429 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to SDAA_ECOLI gi|1788116 percent identity 77 in 455 aa, similar to SDAB_ECOLI gi|1789161 percent identity 99 in 455 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DD 161304 TCAATATACTACTCGTGTTTTAAAAGCGCCAAAAACCATACCACAGCAAGAAGAACT 161363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 161364 ACGCCGCCCAGGTGACCAGCGCCAGCAACCACGCGACTGCATCAATAACGCGCTACCA 161423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 161424 CCAAAAATCCCCGCGCAAATCAGGACCAAATCGCTGATAGCGCAAAGTAAGGCAATCATA 161483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis H37Rv complete genome; segment 89/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 tocaccttgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 atgccaccccagcgcataatatcgagcacgatcggcgcggcattggacaaaagatcaacg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atgagtccttcgcgcttaattccttgtttaatcaccagtacattctgcggtccgatggac 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                      /evidence=not_experimental
/product="probable serine transporter"
/protein_id="BAB37079.1"
/db_xref="GI:13363128"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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7285. .8652
938. .7227
'qene="ECs3656"
                                                                                       /gene="ECs3656"
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Z74025.1 GI:326
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VERSION
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/db_xref="SWISS-PROT:010837"
/db_xref="SWISS-PROT:010837"
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TVASCPUTRIVLGGYSQGAVYLDLGSTSAMPPAVADHYAAVALFGEPSGFSSMWGGG
SLPTIGPLYSSKTINLCAPDDPICTGGGNIMAHVSYVQSGMTSQAATFAANRLDHAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jobes 1879 (MTC739.34), len: 303, LysR family member similar to many regulatory proteins, especially ICIA_ECOLI P24194, chromosome initiation inhibitor, (297 aa), and P94632 LYSTNE RXPORT REGULATOR PROTEIN. (290 aa). FASTA scores, P94632 LYSINE EXPORT REGULATOR PROTEIN opt: 705 coverlap; and ICIA_ECOLI P44194 opt: 520, z-score: 632.5, E(): 1.1e-28, (35.8% identity in 288 aa overlap; and ICIA_ECOLI P44194 opt: 520, z-score: 632.5, E(): 1.1e-28, (35.8% identity in 285 aa overlap); contains signature. Also contains helix turn-helix motif at aa 22-43, (+5.52 SD)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
CUTI_ALTBR P41744 cutinase precursor, (209 aa) FASTA scores, opt: 283, z-score: 3220, E(): z.2e-11, (32.6% identity in193 aa overlap). Also similar to M. tuberculosis Rv3452, Rv3451, Rv2301, Rv1758, Rv3724."
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                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Rv1984c"
/note="PS00155 Cutinase, serine active site"
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                                                                                                           /codon_start=1
/transl_table=11
/product="hypothetical protein Rv1984c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein Rv1985c"
/protein_id="CAA98410.1"
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Pred. No. 2.3e-07;
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Sequence 15 from Patent EP1016710.
AX030085
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5739. .6650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv1985c"
complement(5739. .6650)
/gene="Rv1985c"
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55.0%;
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                                                                                                                                                             /db_xref-"swiss-prot.010840"

/db_xref-"swiss-prot.010840"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YY IFATYTTTVDFGNGIVTAPTAVNVVLLSIPTSPFAISTYFSALLADPTTTPFEAYF
GAVGVDGVLGVGPNAVGPGPSIPTMALPGDLNQGVLIDAPAGELVFGPNPLPAPNVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv1984c, (MTCY39.35), len: 217. Probable cutinase
precursor with N-terminal signal sequence, , similarity to
                                                                                                                                                                                                                                                                        ESFLFYSGFYLPMYWSSRGKLTNTADLIRLIIRDEAVHGYYIGYKCQRGLADLTDAER
ADHREYTCELLHTLYANEIDYAHDLYDELGWTDDVLPYMRYNANKALANLGYQPAFDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSACLIGNGGAGGAGGPNAPGGAGGNGGWLLGNGGIGGPGGASSIPGMSGGAGGTGG
AAGLLGWGANGGAGGLGDGVGVDRGTGGAGGRGGLLYGGYGVSGPGGDGRTVPLEIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTEPTVHANVNGGPTST1LVDTGSAGLVVSPEDVGG1LGVLHMGLPTGLS1SGYSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGSPITTLYVKIDGGTPIPVPSIIDSGGVTGTIPSYVIGSGTLPANTNIEVYTSPGGD
RLYAFNTNDYRPTVISSGLMNTGFLPFRFQPVYIDYSPSGIGTTVFDHPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rv1983, (MTCY39.36c), len: 558; Member of M. tuberculosis PE_PGRS family. Contains PS00141 Bukaryotic and viral appartyl proteases active site; similar to MTCY130.10c, (43.3% identity in 522 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-Rv1982, (MTCY39.37), len: 139, Similar to Mycobacterium tuberculosis Z92772|MTY20H10_5 (131 aa) FASTA scores: opt: 288 z score: 388.5 E(): 4.1e-14; 40. identityin 127 aa overlap, also similar to Rv2759c, and Rv0609*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3871. 3906
/gene="PE_BGRS"
/note="PS00141 Eukaryotic and viral aspartyl proteases
                                                                                                                                                                                                                                                                                                                                                                                                             'note="PS00368 Ribonucleotide reductase small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2981. ....2985
/note="ggagg, potential rbs upstream of Rv1983"
2992. .4668
/gene="PE_GGS"
2992. .4668
/gene="PE_PGRS"
/note="Rv1983, (MTCY39.36c), len: 558; Member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1946. .1949)
/note="agga, potential rbs upstream of Rv1981c"
complement(2161. .2580)
/gene="Rv1982c"
                                                                                                                                                                                                                                                                                                                           DTCQVNPAVRAALDPGAGENHDFFSGSGSSYVMGTHQPTTDTDWDF" complement(1589. .1636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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/db_xref="SWISS-PROT:Q10874"
     reductase small subunit signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SWISS-PROT:Q10873"
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                                                                                                                                    /db_xref="GI:1403474
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                                                                                                                                                                                                                                                                                                                                                                                      /gene="nrdF"
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                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MDGFHHYNSWLDAHQLRPFKGAPETFDVAKLTENLRQVVEGDCT"
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YGSREHGEAHIAAGAKKVLFSHPGSNDLDATVVYGVNQDQLRAEHRIVSNASCTTNCI
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ITRFFPQFNDRFEAIAVRVPTINVTALDLSVTVKKPVKANEVNILLLQKAAQGAFHGIV
DYTELPLVSVDFNHDPHSAIVDGTQTRVSGAHLIKTLVWCDNEWGFANRMLDTTLAMA
TVAFR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="glyceraldehyde 3-phosphate dehydrogenase (AA-339)"
                                                               (28-JUN-1989) by Alefounder P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAMLYDALKAMKFADFSVWSEARFSGMVKTA"
                                                                                                                                                /organism="Escherichia coli"
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        J. 257 (2), 529-534 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292. .303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            718. .729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1881. .1906
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1915. .1942
/note="inverted repeat D'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="inverted repeat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648. .657
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                                                                                                                                                                                                                                                                                                                     /note="ORF1 (AA 1-95)"
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                                                                                                                                                                          /strain="CS520"
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        Biochem. J. 257 (2),
89193446
Data kindly reviewed
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                                                                                                                                                                                                                                                                                           142. .429
                                                                                                                   1. .8029
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                                     MEDLINE
           JOURNAL
                                                                                            FEATURES
                                                                                                                                                                                                                                                                                           CDS
                                                                     COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 4376 to 5508)
Alforounder, P.R., Baldwin, S.A., Perham, R.N. and Short, N.J.
Cloning, sequence analysis and over-expression of the gene for the
class II fructose 1,6-bisphosphate aldolase of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 atgccaccccagcgcataatatcgagcacgatcggcgcggcattggacaaaagatcaacg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 ACGCCCCCAGGTGACCAGCCCAGCAACCACGCCGACTGCATCAATAACGCGCTGCCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atgagteettegegettaatteettgtttaateaceagtaeattetgeggteegatggae 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 TCAATATTACTGCTCATTGCTGTTTTAAAAGCGCCAAAACCATACCACACAGCAAGAGGCT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 ATGTGGTACTGACGACGTATGCCCTGATTCATCACAAAAGCATTTTGTGGACCGAGCGGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-1994
1 (bases 1 to 636)
Nakanishi,K., Aleshin,V.V., Livshits,V.A., Tokhmakova,I.L.,
Troshin,P.V. and Zaskatewey,N.P.
Wethod for producing 1-amino acids
Patent: EP 1016710-A 15 05-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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Escherichia coli fda, pgk and gapB genes for fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.4; DB 9; Pred. No. 2.2e-07; 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 agtaaaagactggcccccaaaagcagacctgtaatgaa 326
                                                                                                                                                         1. .636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJINOMOTO KK (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
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1 (bases 1 to 8029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 51.1
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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ECFDAPGK/C
LOCUS
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Blattner, F.R.
Direct Submission
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Blattner, F.R.
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Escherichia coli K12
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VLETAAKVKAPVIVQFSRQASFIAGKGKKENDVQGAALICAISGAHHUQNAEHYG
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YLERWSKIGWTLEICHGGEBDGVDNSHMOASALYTQPEDVDYAYTELSKISPRFY
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DSVSYGVVKNNIDTDTQWATPPTLLNSQEYVSKKHNLPHNSLNFYFHGGSGSTRQEIK
LRAGQTSMIARLEKAPOELNAIDVL"
                                                                                                                                                           ELALKQGAKVMVTSHLGRPTEGEYNEEFSLLPVVNYLKDKLSNPVRLVKDYLDGVDVA
EGELVVLENVRFNKGEKKDDETLSKKYAALCDVFVMDAFGTAHRAQASTHGIGKFADV
                                                                                                                                                                                                ACAGPLLAAELDALGKALKEPARPMVAIVGGSKVSTKLTVLDSLSKIADQLIVGGGIA
                                                                                                                                                                                                                   NTFIAAQGHDVGKSLYEADLVDEAKRLLTTCNIPVPSDVRVATEFSETAPATLKSVND
VKADBQILDIGDASAQELAEILKNAKTILWNGPVGVFEFPNFRKGTEIVANAIADSEA
FSIAGGGDTLAAIDLFGIADKISYISTGGGAFLEFVEGKVLPAVAMLEERAKK"
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AGLAVGLAGGSLSNILAGVILVMFRPRAGETVDLGGVAGTVLSVQIFSTTMRTADG
KIIVIPNGKILGGSLSNILAGRPVRRNĒFILGVAYDDIOVKQILTNILGSEDRILKD
REMTVRLNELGASSINFVYRVWSNSGDLQNYVWDVLERIKREFDAAGISFPYPODMUN
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SALLMQSPWLLALVPWGQVAFLLWYGFGFRWANSXHIELASAEVMKQGRWKIIATML
AVTWLNPHYYLDTFYVLGSLGGQLDVEPKRNFALGTISASFLWFFGLALLAAWLAPRL
RTAKAORIINLVVGCVWWFIALQLARDGIAHAQALFS"
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1922 c 2114 g 2009 t
                                                                                                                                      /translation="MSVIKMTDLDLAGKRVFIRADLNVPVKDGKVTSDARIRASLPTI
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/note="fructose 1,6-biphosphate aldolase (AA 1-359)"
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                  phosphoglycerate kinase (AA 1-387)"
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/note="inverted repeat E"
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/db_xref="GI:41424"
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/note="ORF4 (AA 1-197)"
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/note="ORF5 (AA 1-197)"
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/note="ORF6 (AA 1-155)"
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Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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This sequence was determined by the E. coll Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director) Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coll K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
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Escherichia.
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                                                                                                                                                                                                                                                                                        109 atgccaccccagcgcataatatcgagcacgatcggcgcggcattggacaaaagatcaacg 168
                                                                                                                                             49 tecacettgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
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Length 8029;
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   DB 2;
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Escherichia coli K12 MG1655 section 265
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SALHILRRKYDEWQPRVLTCSALEKRGIDEIWHAIIDFKTALTASGRLQQVRQQQSVE
WLRKQTEEEVLNHLFANEDFDRYYRQTLLAVKNNTLSPRTGLRQLSEFIQTGYFD"
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NLTRDAGFHVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMAHHISEKAPL
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5150. .6628
/gene="ygfh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA IMPYCGNTLRLGVTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
GDKTRMNDLARAEAAFIRPVPSSGHLGGASQRARELMLLCEAAGYDVVIVETVGVGQS
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VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWLTSGIGNAPTWLLRAKKVIIE
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YDPFMWYSEVLQESVYHLLETGKISGASASSLTISADSLKRIYDNMDYFASRIVLRP
QEISNNPEIIRRLGYALNVGLEFDYYGHANSTHVAGVDLMNGIGGSGDFERNAYLSI
FMAPSIAKEGKISTVVPMCSHVDHSEHSVKVIITEQGIADLRGLSFLQRARTIDDNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MINEATLAESIRRLRQGERATLAQAMTLVESRHPRHQALSTQLL
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                   AGSYYIESLTDQIVKQARAIIQQIDEAGGMAKAIEAGLPKRMIEEASAREQSLIDQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNLSRRNILIKGIFMSYQYVNVVTINKVAVIEFNYGRKLNALSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative enzyme; Not classified"
/note="0275; This 275 aa ORF is 30 pct identical (6 gaps)
to 250 residues of an approx. 296 aa protein ECHW_RAT SW:
p14604"
                                                                                                                                                                                                                                                                                              3335. .4330
/gene="ygfD"
/function="phenotype; Not classified"
/note="0331; 100 pct identical to YGFD_ECOLI SW:
P27254(157 aa) but has 25 additional N-ter aa 50
additional C-ter aa; orf2 of X66836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"putative nucleotide-binding protein"
/protein_id="AAC75955.1"
/db_xref="GI:1789285"
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/protein_id="AAC75957.1"
/db_xref="GI:1789287"
                                                                                                                                                                             LQERGVAAIYGPGTPMLDSVRDVLNLISQHHD"
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/product="putative enzyme"
/protein_id="AAC75956.1"
/db_xref="G1:1789286"
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/gene="ygfI"
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/transl_table=11
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3335, .4330
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/gene="ygfG"
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/gene="ygfH"
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/gene="ygfG"
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30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CS Site Nos., unique ID nos. for the genes in the E. coil Genetic. Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web Site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MRRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN
MRGQPLLVREVPPRPTEOGGKLLALLRQVELLEEBRIGDEOTGSTPLILSIAVNADSI'
MTHLIPALAPVLADSPIRTNIQVEDETRIQERLRRGEVVGAVSIQHQALPSCLVDKLG
ALDYLFVSSKRFABEYFPNGYTRSALLKAPVVAFDHLDDMHQAFLQQNFDLEPGSVPC
HIVNSSEAFVQLARQGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
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FGIGMDLFMNVAMLRAARYLWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV
IRTTIEALAATLGGTQSLHTNAFDEALGLPTDFSARIARNTQIIIQEESELCRTVDPL
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SVAFDLATHRGYDSDNPRVAGDVGRAGVAIDTVEDMKVLFDQIPLDKMSVSMTMNGAV
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/note="factor Sigma70; predicted +1 start at 3057674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="factor Sigma70; predicted +1 start at 3057742"
101. .994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'function="regulator; DNA - replication, repair,
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/protein_id="AAC75954.1"
/db_xref="GI:1789284"
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/db_xref="G1:1789283"
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/transl_table=11
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/gene="iciA"
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/gene="iciA"
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/gene="sbm"
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'qene="sbm"
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NDAQRQAVEGMKPFFGVQAGDLFIATTGYTGEAGYEIALPNEKAADFWRALVEAGVKP
                                                                                                                                                                                                         /translation="MAIALVTGGSRGIGRATALLLAQEGYTVAVNYQQNLHAAQEVMN
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IVPKDIQLATPPQVGAPATEYAALAELKAIASRNKRFTSYIGMGYTAVQLPPVILRNM
LENPGWYTAYTPYQPEVSQGRLEALLNFQQVTLDLTGLDMASASLLDEATAAAEAMAM
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MQPNSGAQGEYAGLLAIRHYHESRNEGHRDICLIPASAHGTNPASAHMAGWQVVVVAC
DKNGNIDLTDLRAKAEQAGDNLSCIMVTYPSTHGVYEETIREVCEVVHQFGGQVYLDG
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FKIKASDESELESLLDATAYEALLEDE"
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GTEKLVGLVMTEKGVLRNELPVRFTDAQGNQHEGIITSGTFSPTLGYSIALARVPEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANMNAQVGITSPGFIGADVSHLNLHKTFCIPHGGGGPGMGPIGVKAHLAPFVPGHSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q.I.EGMLTRQGAVSAAPFGSASILPISWMYIRMMGAEGLKKASQVAILNANYIASRLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFPVLYTGRDGRVAHECILDIRPLKEETGISELDIAKRLIDYGFHAPTMSFPVAGTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEPTESESKVELDRFIDAMLAIRAEIDQVKAGVWPLEDNPLVNAPHIQSELVAEWAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAQQTPLYEQHTLCGARMVDFHGWMMPLHYGSQIDEHHAVRTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMFDVSHMTIVDLRGSRTREFLRYLLANDVAKLTKSGKALYSGMLNASGGVIDDLIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(318. 3634)
//note="similar to Genbank Accession Number L20872" (ECGCCWHP); bases 3318 to 3438 differ from the sequence presented here, as well as from X73958 and D21144"
                                                                                                                                                                                                                                               LITQAGGKAFVLQADISDENQVVAMFTAIDQHDEPLAALVNNAGILFTQCTVE
                                                                                                                                                                                                                                                                                         complement(1. .5335)
/note="similar to GenBank Accession Number X73958
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GenBank Accession Number D21144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GenBank Accession Number M97263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSREVAVFPAGVADKYWPTVKRLDDVYGDRNLFCSCVPISEYQ'
                                                                                                                 /protein_id="AAA69070.1"
/db_xref="G1:882432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAA69071.1"
/db_xref="GI:882433"
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/db_xref="G1:882434"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA69073.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3551. .3940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3964. .5058)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3964. .5058)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3551. .3940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(559. .3432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:882435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (3809.
                                                                                    l_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="gcvP"
/note="ORF_f957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="gcvH"
/note="ORF_f129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                      complement(70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                             complement(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="gcvP'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ECOPYU18)"
                                                                                                                                                                                                                                                                                                                                                                     (ECGCVOP)
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/function="putative regulator; Not classified"
/note="f303; This 303 aa ORF is 25 pct identical (11 gaps)
to 241 residues of an approx. 304 aa protein CYNR_ECOLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined as part of the E. coli Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655, overlaps with other sequence determinations are annotated. This entry should be considered somewhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provisional; it will be updated and merged with others at a later
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 87107)
                                                                                                                                                                                                                                           /product="putative transcriptional regulator LYSR-type"
/protein_id="AAC75958.1"
/db_xref="G1:1789288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8867 TCAATATTACTGCTCATTGCTGTTTTAAAAGCGCCCAAAACCATACCACAGCAAGAAGGCT 8926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 tccaccttgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 atgccacccagcgcataatatcgagcacgatcggcgcggcattggacaaaagatcaacg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 atgagteettegegettaatteettgtttaateaceagtaeattetgeggteegatggae 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1995
68 minutes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                      Length 10362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECU28377 141744 bp DNA BCT
Escherichia coli K-12 genome; approximately
U28377
                                                                                                                                                                                                                                                                                                                                                                                                      Score 60.4; DB 1; I Pred. No. 4.1e-07; 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9107 AGGATCATAGCCGCCCCAAGTGCAAGACCTTGAAAGTA 9144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agtaaaagactggccccaaaagcagacctgtaatgaa 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'sub_strain="MG1655"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.5%;
Best Local Similarity 51.1%;
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U28377.1 GI:882431
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                                                                                                                              SW:
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AUTHORS
TITLE
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/translation="msaqpydigifgrslryncppdqrdalnqaaddlnqrlgdlkrr
trytnteglyfiaalnisyelaqeraktrdyaasmeqrirmlqqtieqalleggrite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 tecacettgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                 /product="stable 6S RNA"
10374. .10556
/gene="ssr"
10374. .10557
/note="similar to GenBank Accession Number X01238
(ECRRN6S)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 atgccaccccagcgcataatatcgagcacgatcggcgcgggcattggacaaaagatcaacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca
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                                                                                                                                                           10266. .11219
/note="similar to GenBank Accession Number M12965
/RCOSSR\"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.5%; Score 60.4; DB 2; Length 141744; 51.1%; Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23150 AGGATCATAGCCGCCCCAAGTGCAAGACCTTGAAAGTA 23187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agtaaaagactggcccccaaaagcagacctgtaatgaa 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 14, 2001, 07:52:13
Job time: 15035 sec
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                                                                                                                                                   KTNONFE"
                                                                                                                                                                             misc_feature
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WONSDFWYFTGFNEPEAVLVLIKSDDTHNHSVLFNRYRDLTAEIWFGRRLGQDAAPEK
LGVDRALAFSEINQQLYQLLGLDVYVHAGGEYAYADVIVNSALEKIRKGSRQNLTAP
ATMIDWRPVYHEMREFKSPEEIAVLRRAGEITAMAHTRAMEKCRPGWFEYHLEGEIHH
EFNRHGARYPSYNTIVGSGENGCILHYTENECEMRDGDLVLIDAGGEYKGYAGDITRT
                                                                                                                                                                                                                                                                                                                                                                                                   IGADGANSWLRNKADIPLIFWDYQHHALVATIRTEEPHDAVARQVFHGEGILAFLPLS
PHLCSIWWSLSPEEAQNWQQASEDEPRALMATBODNAGLGKVFESAROYPPLIGRYA
RQFRSHRLALVGDAHTIHPLAGGGVNLGFWDAAELIAELKRLHROGKDIGOYYYLLRR
YERSRKHSAALMLAGWQGFRDLFSGTNPAKKLLRDIGLKLADTLPGVKPQLIRQAMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCSLVWCHPLERREEVLSWSDEKFCRELQSAFGWRLGKITHAGKRSAYPLALFHAARS
ITHRTVLVGNAAQTLHPIAGGGFNLGMRDVMSLAETLTQAQERGEDMGDYGVLCRYQQ
RRQSDREATIGVTDSLVHLFANRWAPLVVGRNIGLMTMELFTPARDVLAQRTLGWVAR
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DSSWLPLLTNEGMAFGFELAQALKKHGSATSDALQDDGFLFQLYLDGGDDVSVFD
RADALAGWVNHFLLGLGVYQPKLDKVTGFTGEATDDLRNIAQLGYDEDDGELEMSL
EBIIEVYRVAALLCGIDFFTHROPTABEVQKPPLH"
                                                                                                                                                                                                                                                                                                                                                   PPQLRVSAINAASEKLLTRLGVWQDILSRRASCYHGMEVWDKDSFGHISFDDQSMGYS
HLGHIVENSVIHYALWNKAHQSSDITLLAPAELQQVAWGENETFLTLKDGSMLTARLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDGRAIALAAGTCQQLARIGVWQSLADCATAITTVHVSDRGHAGFVTLAAEDYQLAAL
GQVVELHNVGQRLFALLRKAPGVTLHCPDRVANVARTQSHVEVTLESGETLTGRVLVA
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DVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYGQDRSRILEPGMVLTVEPGLYIAPD
                                                                                                                                                                                                                                                                                                                              /translation="MQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEQRVQEPLAANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to GenBank Accession Number D00398 (ECOAPP2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEVPEQYRGIGIRIEDDIVITETGNENLTASVVKKPEEIEALMVAARKQ
                       complement(5370. .10317)
/note="similar to GenBank Accession Number D90281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-"ORF_f441; third start codon"
GETAIVQIRNREMPVKVTKPVFVRNGKAVA"
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/db_xref="GI:882438"
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/db_xref="G1:882437"
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/db_xref="GI:882439"
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                                                                                                 complement(5506. .6708)
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                                                                                                                                                                                                note="ORF_f400"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stover, Charles K.
APPLICANT: Stover, Charles K.
APPLICANT: Mahalras, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 63.2; DB 1; Length 1
55.3%; Pred. No. 3.3e-10;
tive 0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGRYT INFORMATION:
NAME: HUNTER: TOM
US-08-438-862-4
US-09-124-671-24
US-09-001-982-11
US-09-001-982-11
US-09-076-193-6
US-08-073-303-3
US-08-073-303-5
US-09-073-303-3
US-09-073-303-5
US-09-073-303-5
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-155-16
US-09-128-155-16
US-08-465-175A-10
US-08-465-655-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08390878
; Patent No. 5700683
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
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Matches 166; Conservative
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STATE: California
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/cgnl_7/ptodata/1/ina/5B_COMB.seq:*
/cgnl_7/ptodata/1/ina/6A_COMB.seq:*
/cgnl_7/ptodata/1/ina/6B_COMB.seq:*
/cgnl_7/ptodata/1/ina/PcTuS_COMB.seq:*
/cgnl_7/ptodata/1/ina/PcTuS_COMB.seq:*
                      4.5
Compugen Ltd.
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                                                                                                                                                   September 14, 2001, 04:24:46; Search
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US-08-685-6284-5

US-08-685-315-33

US-09-265-315-33

US-09-265-315-33

US-09-265-315-33

US-09-265-315-33

US-09-265-315-33

US-09-150-460B-9

US-09-150-460B-9

US-08-173-900-1

US-09-385-028-21

US-09-385-028-13

US-09-385-028-13

US-09-385-028-13

US-09-385-028-13

US-09-386-028-13

US-09-386-028-13
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   US-09-105-117I-1_COPY_1016_1726
                                                                                                                                                                                                                                                                                                                                                                                        324599 segs, 94655562 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                        GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
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Match Length DB
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1299
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Maximum DB
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                                                                                                                          5373 CAGGTGCTGGTGGTCAGGGAAAAGCCATGTCGGGCGACGACGCAGGTATCCCGCTGTTG 5432
                                                                                                                                                                                                                                                                             5493 GCGTCGCTGAAACGCACCCGGATCACCATTGCGGTAAACGCCGATTCCATGGCGGACATGG 5552
478 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kaphammer, Bryan J.
TITLE OF INVENTION: tfdA Gene Selectable Markers in Plants and the
TITLE OF INVENTION: Use Thereof
                                                                                                                                                                  598 caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                       5313 CTACATGTCACCCCTCGGCTGTCAGTCAGTCGATCGTTGGAGCAGCAGGTCGGC
                                                                                                                                                                                                                                                       gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
                                                                                   538 cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                                                                                            5433 CGGTTGGCCGCGAAACAGCGTTGCTCGAGTCCGAGGCGCTTCGCTGAAATGGGTGGCAAC
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Pred. No. 0.035;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANUKESSEE: Sterne, Ressler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1405.0030001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,117
FILING DATE: 15-DEC-1994
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
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Sequence 1, Application US/08358117

Patent No. 5608147

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2058 harr
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.2%;
Best Local Similarity 53.9%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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751..1611
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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2,4-DICHLOROPHENOXYACETIC ACID (2,4-D) MONOOXYGENASE FORMATION AND PROCESS FOR THE PRODUCTION OF THESE PLASMIDS AND STRAINS
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Pred. No. 0.035;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                              FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470 From
                                                                                                                                                                                                      MICROORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-685-625A-5; Sequence 5, Application US/08685625A; Patent No. 5945301
                                                                                        Sequence 1, Application US/08470588 Patent No. 6100446
                                                                                                                             GENERAL INFORMATION:
APPLICANT: STREBER, WOLFGANG R.
APPLICANT: TIMMIS, KENNETH N.
APPLICANT: ZENK, MEINHART H.
410 GIGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LAMENCE, WILLIAM F.
REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 GIGITGITGITCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) MOLECULE TYPE: DNA (genomic) US-08-470-588-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                745 FIFTH AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2058 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.2
Best Local Similarity 53.9
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212-588-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                              TITLE OF INVENTION: MITTITLE OF INVENTION: 2
TITLE OF INVENTION: F
TITLE OF INVENTION: F
TITLE OF SEQUENCES: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                         10151
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                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                         US-08-470-588-1/c
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                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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292 aaaagactggcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacc 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 32.8; DB 3; Length 1876;
48.3%; Pred. No. 0.77;
ive 7; Mismatches 68; Indels 0
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                                                                                                                                                             STATE:
COUNTRY:
U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Malouin, Francols
APPLICANT: Malouin, Francols
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222/005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 322/
RELECOMMUNICATION INFORMATION:
TELEPAN: (213) 489-1600
TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.3
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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            CORRESPONDENCE ADDRESS ADDRESSE: Lyon & Ly
                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-265-315-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-714-918-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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GENERAL INFORMATION:
APPLICANT: UBNO, Nacto
APPLICANT: UBNO, Nacto
APPLICANT: UBTSUNOTO, Kunihiro
APPLICANT: INTE, Wenji
TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
TITLE OF INVENTION: TRANSDUCTION SYSTEM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
CITY: Alexandria
STREET: P.O. BOX 1404
STREET: P.O. BOX 1404
CITY: BLOYDIAGE
STREET: P.O. BOX 1404
STREET: P.O. BOX 1404
CITY: BLOYDIAGE
STREET: P.O. BOX 1404
STREET: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.79;
..hes 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
GENERAL INFORMATION:
BENCON:
APPLICANT:
Schmid, Molly B.
APPLICANT:
SUN, DONGAU
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 2
Pred. No. 0.79;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     001560-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 43.5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-253549
FILING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: MEUTh, DOING M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-2
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2656 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1324 CAACCTCTGAGGGCAAGAGGA 1344
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Best Local Similarity 63.0%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183..1922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-685-625A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-714-918-33
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292 aaaagactggcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacc 351
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APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
4.6%; Score 32.8; D:
Best Local Similarity 48.3%; Pred. No. 0.77
Matches 70; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTONNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 cccattcaactggacactttgctct 436
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Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                           Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
       CORRESPONDENCE ADDRESS:
                                         ADDRESSEE: Lyon & I
STREET: 633 West Fi
STREET: Suite 4700
                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1876;
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APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Prancois
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREBNING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.6%; Score 32.8; DB 4;
Best Local Similarity 48.3%; Pred. No. 0.77;
Matches 70; Conservative 7; Mismatches 68;
ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 814 # 4700 CITY: Los Angeles STATE: Callfornia COUNTRY: U.S.A. ZIP: 90071-2066 COMFUTEN READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/265,315
FILING DATE: MArch 9, 1999
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICE.
FILING DATE: Ser-
ATTORNATION.
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
TELEX: (57-3510
TELEX: (57-3510
TELEX: (57-3510
TELEX: (57-3510
TELEX: (67-3510
TENEY: (67-3510

                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 cccattcaactggacactttgctct 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-09-265-315-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-265-315-33
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165 aacgeecaaggtgeeggegatgaacaaaaagaegteagaaattaaacacaegagaagaae 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 agcgatgccaccccagcgcataatatcgagcacgatcggcgggcattggacaaaagatc 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 AGGGGGGCCTGGCGAGGGGACGCCATCATGCACACTCGCTGCTGTGGAGCTGAGATC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian Circadian Rhythym-Like Gene
                                                                                                                                               Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.2; DB Pred. No. 0.85; 0; Mismatches
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APPLICANT: Lee, Cheng-Chi
APPLICANT: Lee, Cheng-Chi
APPLICANT: Eichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION: Mammalian Circadian Rhytl
FILE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 9
                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
CLASSIFICATION DATA:
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE91/01020
APPLICATION NUMBER: PCT/DE91/01020
PRIOR APPLICATION NUMBER: DE 40 41 304.7
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: DE 40 41 304.7
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6136527man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LEDER 201
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ. ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 cgcaatgagtccttcgcgcttaattcct 252
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: 805 Third Avenue
New York City
                                                                                                                                                                                                PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                       SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                     Wordperfect
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                      IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 75; Conserva
                                                                                                                                                                                              OPERATING SYSTEM:
                                                   New York
                                              STATE: New COUNTRY: US ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4700
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Patent No. 6136527
GENERAL INFORMATION:
APPLICANT: Fuchs, Klaus; Motz, Manfred; Roggendorf, Michael;
APPLICANT: Soutschek, Erwin
TITLE OF INVENTION: Polypeptides Derived from Proteins of the
TITLE OF INVENTION: Polypeptides Derived from Proteins of the
TITLE OF INVENTION: and Vaccines against Infection by Hepatitis C Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666 AATGGTTTGAGATATKTCGACAGTTTGGTTWTTTACCTGGATTTATATTTATATTA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 aaaagactggcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacc 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.8; DB 4; Length 1876;
Pred. No. 0.77;
7; Mismatches 68; Indels 0
                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETTE, 1.00 SCOMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: MARCH 9, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240/248
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                                                3E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 24(
IELECOMMINICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.3%;
Matches 70; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & L
                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-078-271B-9
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Query Match
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                                                                                                                                                                                3117 ccccaccgcccagactccccactgttcaactcgagatgcagctccccactccagctcaa 3176
             Nucleotide sequence of m-rigul, a murine brain cDNA homologous to a human RIGUI 4.7 cDNA probe
                                                                                                                                                             451 ggcagcttcgaaggcgcctccttagccctttccatttccccctcggcggtgagtcagcgc 510
                                                                                                                                                                                                                              511 gttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcacccaaccggccaaa 570
                                                                                                                                 Gaps
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                                                                                             DB 4; Length 4700;
                                                                                            Score 31; DB 4; Length 470
Pred. No. 4.7;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                571 gcaaccgaagcgggtgaagtccttgtgcaagcagcgcgg 609
                                                                                                                                                                                                                                                                                                                                                                                                                                           NERAL INFORMATION.
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND STREET 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                             4.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7218 base pairs
                                                                                                           Best Local Similarity 49.79
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 7218 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
           ) OTHER INFORMATION:
) OTHER INFORMATION:
US-09-150-460B-9
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           US-08-232-463-14/c
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                                                                                             Query Match
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1070 RRRRATCGCAAGCTCCCTCGACCTGCAGCTCGGAATTAATTCTGTGAGCGTATGG 1011
                                                                                                                                  84 gacggcaaaccataacaggtaagcgatgccaccccagcgcataatatcgagcacgatcgg 143
                                                                                                                                                                                                 144 cgcggcattggacaaaagatcaacgcccaaggtgccggcgatgaacaaaaagacgtcaga 203
                                                                                                                                                                                                                                                                                                204 aattaaacacacgagaagaaccgcaatgagtccttcgcgcttaattccttgtttaatcac 263
                                                                                                                                                                                                                                                                                                                                                                                                 264 cagtacattctgcggtccgatggacagtaaaagactggcccccaaaagcagacctgtaat 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 taacatggtttaatatagcttcatgaaccccattcaactggacactttgctctcaatcat
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APPLICANT: CAMERON, Beatrice
APPLICANT: CROUET, Joel
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
4.4%; Score 31; DB 1; Length 7218; 14.2%; Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                   Conservative 140; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01178
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: FR 94/11049
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Savitzky Esq., Martin F.
REGISTATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94069-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,900
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08793900 Patent No. 6143518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collegeville
                    Best_Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 tgatgaa 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                            RESULT 14
US-09-385-028-13/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                             δλ
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                                                                                                                                                                                                                                    508 cgcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcacccaaccggcc 567
                                                                                                                                                                                                                                                                                                                 568 aaagcaaccgaagcgggtgaagtccttgtgcaagcagcgcggaaaatggtgttgctgcaa 627
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
                                                                                                                                                                                               ö
                                                                                                                                                         Length 8501;
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STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
STATE: D.C.
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                               57;
                                                                                                                                                       Score 30.8; DB 3;
Pred. No. 7.4;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF INVENTION: Acid Biosynthesis R OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALGENEL D. DOUGHAS PLICE
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-666
TELEFAX: (202) 39305350
TELERX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-09-385-028-21
                                                                                                                                                       Query Match
Best Local Similarity 53.3%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
8501 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
WOLECULE TYPE: CDNA
US-08-793-900-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                           284 ACGGCAGCATCAACCGGGCCGCGGGGGTGCTGTCGATCAGCCAGTCGGCGCTCACCCGCC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 aaggcagcttcgaaggcgcctccttagccctttccatttccccctcggcggtgagtcagc 508
                                                     Gaps
                                                                                                                                                                                                                 509 gogttaaagototogagoatoacgtgggtcgagtgttggtatcgcgcacccaaccgg 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11604;
Length 1299;
                                                54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
  Score 30.6; DB 4;
Pred. No. 3.3;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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4.3%; Score 30.6; Di
Best Local Similarity 53.8%; Pred. No. 10;
Matches 63; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS PTICE
REGISTATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09385028 Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELERA: (202) 39305350
TELEX: CAC 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) US-09-385-028-13
    4.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Susan E. Jensen
    Query Match 4.3
Best Local Similarity 53.8
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Susan
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9189 GGATTCACCGGCTGGAGCAGTCCCTCGGCGCCCGGCTGCTGCTGCGGCGAGCCCGCGGG 9133
                                                                                                                                                                                                      APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TILE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STRET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1418/P57452US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452
TELEPHONE: C.022 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces clavuligerus US-09-385-028-1
                                                                           RESULT 15
US-09-385-028-1/c
; Sequence 1, Application US/09385028
; Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TREEFORMS (202 838-6666 TELEFAX: (202) 39305350 TELEX: RCA 248593 IDEA UR INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 15079 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Single
TOPOLOGY: linear
MODECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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СP
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ö 449 aaggcagcttcgaaggcgcctccttagccctttccatttcccctcggcggtgagtcagc 508 Gaps 4.3%; Score 30.6; DB 4; Length 15079; 53.8%; Pred. No. 11; tive 0; Mismatches 54; Indels 0; Query Match
Best Local Similarity 53.8 Matches 63; Conservative ò

Db 11281 ACGCCACCATCAACCGGGCCGCGGGGGTGCTGTCGATCAGCCAGTCGGCGCTCACCGCC 11222

GGATTCACCGGCTGGACCAGTCCCTCGCCCCGCTGCTGCTGCGCCCGCGCGGG 11165 509 gegitaaagetetegageateaegigggitegagigtitggiategegeaeeegg 565 11221 q ò

Search completed: September 14, 2001, 07:51:13 Job time: 12387 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AL CE RS	TITLE Direct Submitted (28-MAR-2001) BBMI, Institut Pasteur, 25, rue du Dr. JOURNAL Submitted (28-MAR-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France COMMENT This clone is from an A. gambiae BAC library provided by F.H. COllins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut FEATURES Location/Qualifiers	7 /st /st /db /cl /cl /co /no	Ouery Match B.5%; Score 60.4; DB 219; Length 830; Best Local Similarity 50.7%; Pred. No. 8.5e-08; Matches 142; Conservative 1; Mismatches 137; Indels 0; Gaps 0; Qy 43 ggcgcttccaccttgtttgtcatggcgtctttcgctgccatgacggcaaaccataacagg 102	163 tcaecgcccaagtgccggcqatgaacaaaagacgtcagaattaaacacagagaaga 163 tcaecgcccaagtgccggcqatgaacaaaaagacgtcagaattaaacacagagaaga 163 tcaecgccaAAAATCGGGACAGATCAGCAGAAATCACTTACGGGGCATAGCAGGGGA 223 accgcaatgagtccttcgcgcttaattccttgtttaatcaccagtacattctgcggtccg 1	RESULT 2 CNS015QU/C LOCUS LOCUS DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACHAD20 of DrosBAC library from Drosophila melanogaster (fruit ACCESSION AL105792. VERSION AL105792.1 GI:5618347 KEYWORDS GSS SOURCE Fruit fly. ORGANISM Plasmid Drosophila melanogaster	Eukaryota; Medazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Preryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 916) AUTHORS Genoscope. JOURNAL Bull 19106 ENRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr. Bull 19106 ENRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
Description	AL151258 Anopheles AL105792 Drosophil BF128512 601810433 AL223385 Tetracodon BG342366 602374287 A1020087 ubl4c04.r A1174155 v284011.r	AQ104328 AQ405681 HS.5076_A BF485823 AT19875.5 AW851850 RC1-C7019 BF352878 IL3-HT061 AQ851405 LMAJFV1_1 AQ851405 LMAJFV1_1 AQ782619 HS_3183_B AQ782619 HS_3183_B AQ782619 HS_3183_B	A283480 2M0117K13 A283480 2M0117K13 A2834861 2M0117K13 A706549 A7066549 BB565230 BB565230 AA879865 vw01a11.r AA734877 vu64f11.r AA734878 vh28407.r BE290613 601088315 AA065568 m171C07.r	BF01664 uy3401.y BF01664 uy3401.y BF303625 601086274 AW318849 un08d09.y BF37127 601218617 BF282182 601102384 BF719586 mab41h08. BF334431 us/99h09.y BF37573 601229761 AI119048 us931f0.y AQ941109 sheared D BF167006 601774147 WB2115 me98C99.rI WB2115 me98C90.rI	BG174120 BF788835 AK014354 AK014354 31-MAR- 10 22E24	Anopheles gambiae (African ince. ita; Hexapoda; Insecta;
SUMMARIES Result Ouery No. Score Match Length DB ID	60.4 8.5 830 2 40 5.6 916 2 37.2 5.2 2084 1 37 5.2 1018 1 36.4 5.1 409 1 36.4 5.1 473 1	35.8 5.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1	35.2 5.0 3119 2 35.2 5.0 3119 2 35.2 5.0 3119 2 34.8 4.9 4.9 4.59 1 34.8 4.9 4.9 4.59 1 34.8 4.9 4.9 4.9 8 34.8 4.9 4.9 4.9 8 34.8 4.9 4.9 4.9 8 34.8 4.9 4.9 6.9 8 34.8 4.9 6.9 6.9 6.9 8 34.8 6.9 6.9 6.9 6.9 8 34.8 6.9 6.9 6.9 6.9 6.9 8 34.8 6.9 6.9 6.9 6.9 6.9 6.9 6.9 6.9 6.9 6.9	010000000000000000000000000000000000000	34.8 4.9 929 174 BG174120 34.8 4.9 929 174 BG174120 34.8 4.9 1301 192 AK014354 ALICNMENTS ALICNMENTS ALICNMENTS ALICNMENTS ALICNMENTS ALICNMENTS ALICNMENTS ALICNMENTS	library from strain PEST of squito), genomic survey seque GI:7011737 laria mosquito. gambiae Metazoa; Arthropoda; Trachea Neoptera; Endopterygota; Dip; Anopheles. 1 to 830)

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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2084)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/organism="Drosophila melanogaster"
/plssmid="pBeloBAC11"
/db_xref="taxon:7227"
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Plate: LLCM892 row: a column: 09.
Location/Qualifiers
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Best Local Similarity 34.0%;
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TITLE
JOURNAL
COMMENT
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/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI size susing the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
qenome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
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                                     /clone="IMAGE:4053392"
/clone_lib="NIIMAG_46"
//issue_type="leiomyosarcoma cell line"
/lab_host="DH108 (phage-resistant)"
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/organism="Homo sapiens"
                  /db_xref="taxon:9606
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="204B10"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG204DA05LP1-end : T7"
/note="Genoscope sequence ID : C0AG204DA05LP1-end : T7"
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/lab_host="DH10B (phage-resistant)"
/note="Grgan: eye; Vector: pCMV-SPOR76; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full:length clones and constructed by Life Technologies.
In this is a NH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG342366 1018 bp mRNA EST 27-FEB-2001
602374287F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481877 5',
BG342366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                      ggtaagcgatgccaccccagcgcataatatcgagcacgatcggcggcgtggcattggacaaaa 160
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National Institutes of Health, Mammallan Gene Collection (MGC)
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/clone="IMAGE:4481877"
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Location/Qualifiers
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Plate: LLAM10317 row:
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ub14c04.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1366950 5' similar to SW:PRSX_HUMAN Q92524 26S PROTEASE REGULATORY SUBUNIT P42. ;, mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Washi-HHMI Mouse EST Project
Washi-HHMI Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                                                                                                                                                                                       191 AAGTAGCATTCCCCTTTTAAATGTTGGTGTAACATCTTTGTTTTTTATGAAACCAGCTTGA 250
                                                                                                                                                                                                                                                                                                                            311 GAGATATCTGCCAAGAGAGGTGGATCCATTGGTTTATAAACATGTCTCACGAGGATCCTG 370
                                                                                                         228 aatgagteettegegettaatteettgtttaateaeeagtaeattetgeggteegatgga 287
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/tissue_type="macrophage"
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  Length 1018;
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Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 348.
Location/Qualifiers
                                                      Indels
Score 37; DB 152; 1
Pred. No. 2;
0; Mismatches 105;
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/db_xref="taxon:10090"
/clone="IMAGE:1366950"
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The WashU-HHMI Mouse EST Project
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Indels

Length 473;

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Web: www.genoscope.coms.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk ... This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded un Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSO14RI 1100 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACLASC24 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL104520
                                                                                                                                                                                                                            278 gtccgatggacagtaaaagactggcccccaaaagcagacctgtaatgaagatttccatga 337
                                                                                                                                                                                                                                                                                            220 GTCAGCTTGACAAAAGTAAGCTGAAGCCAGGAACCAGAGTTGTTTGGATATGACCACAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ggtaagcgatgccaccccagcgcataatatcgagcacgatcggcggcgtcgttggacaaaa 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1055 GGGVRGMMVGGVGVMMMRGGGGMMMGGGGMMRGVRGAMGGGGGMAGAGRAKGAGAARR 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 tecgatggacagtaaaagaetggeeeceaaaageagaetgtaatgaagattteeatgat 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                            338 tcaccatcgtgacctatggaagtacttaagtaaaatgattggttcttaacatggttta 395
                                                                                                                                                                                                                                                                                                                                                                                             995 NMGAGRAKMMMVMGGGGGMGMKGMGMMMMMMMMMMMMAAAAAKKRAAAADKDAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               935 AAAKKKAAKAAKAAMKKKMMMBMMCMKMMKKKNKKKNKVMWVMMKMNKKMMMMMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 gatcaacgcccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 gaaccgcaatgagtccttcgcgcttaattccttgtttaatcaccagtac--attctgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 others
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                                                                                                                                                                51;
                                                                                                 DB 17;
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                                                                                             Score 36.4; Di
Pred. No. 2.5;
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11.7%; Pred. No. 3.6;
Live 118; Mismatches
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fruit fly.
Plasmid Drosophila melanogaster
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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1. .1100
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/note="end : SP6"
175 c 118 g
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                                                                                                 5.1%;
                                                                                                                                                                67; Conservative
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Direct Submission
                                                                                             Query Match
Best Local Similarity
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CNS014RI/c
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ORIGIN
                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 473)
Marra.M., Hillier.L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary gland; Vector: pT713D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T31; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo. ROMAN STATEMENT STATE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                         278 gtccgatggacagtaaaagactggcccccaaaagcagacctgtaatgaagatttccatga 337
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                        A1174155 473 bp mRNA EST 07-0CT-1998 v284d11.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1333173 5' similar to SW:PRSX_HUMAN Q92524 26S PROTEASE REGULATORY SUBUNIT P42. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                        338 tcaccatcgtgacctatggaagtacttaagtaaaaatgattggttcttaacatggttta 395
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Contact: Marra M/Mouse EST Project
WashU-HMIN Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                             Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seq primer: -28mi3 rev2 ET from Amersham High quality sequence stop: 451. Location/Qualifiers
                                                                                                                                                             Indels
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/sex="male"
                                                                                                                                                             51;
                                                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                             Score 36.4; D
Pred. No. 2.4;
                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
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/clone="IMAGE:1333173"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI174155.1 GI:3720297
                                                                                             5.1%;
                                                                                                                           Best Local Similarity 56.8
Matches 67; Conservative
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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                                                                                                 Query Match
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Length 436;

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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Park, S., Paragas, V., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone=lih="AT Drosophila melanogaster adult testes pOTB7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_grage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/note="Organ: ADULT testes: Vector: pormB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pormB7. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                          BF485823 650 bp mRNA EST 16-APR-2001
AT19875.5prime AT Drosophila melanogaster adult testes poTB7
Drosophila melanogaster CDNA clone AT18975 5 similar to CG13768:
FBan0013768 last_updated:000321, mRNA sequence.
                                                                                                                                          tggtgttgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgt 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AsB003614
Plate: AT.198 row: G column: 3
High quality sequence stop: 633.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 650)
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Pred. No. 4.2;
0; Mismatches 27; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley Drosophila Gene Collection Project
Unpublished (2000)
                                                      37;
5.1%; Score 36; DB 228; 60.6%; Pred. No. 3.2;
                                                                                                                                                                                                                     taaccatcgccatcaacgcagattcgctatccac 707
                                                   0; Mismatches
                                                                                                                                                                                                                                                  127 TCCCCATCCCCATCTTCCTCCATCNCCATCCCC 94
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1. .650
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                                                      Conservative
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                         Similarity
57; Conserv
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                                                                                                          614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                             BF485823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High Throughput Sequencing Center on University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3818
Fax: (206) 616-3888
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 652 row: A column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 436)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ405681 436 bp DNA GSS 13-MAR-1999 HS_5076_A1_A11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=652 Col=21 Row=A, DNA sequence.
NNNWAKMNNNNKTNNNANNKNNNMANNNKNNNKNANNKNTNNKTMMMNNKNNNN 756
                                                                                                                                                                                     399 tagetteatgaaceceatteaactggacaetttgeteteaateattgatgaaggeagett 458
                                                                                                                                                                                                                                                                                                                                                 695 GNGNNNNNAGNAMMANNGNNNNANGTTNTGNNCGCMGNNGNCNNTNNNNNGNNNNNTTGN 636
                                                                                                                                                                                                                          caccatcgtgacctatggaagtacttaagtaaaatgattggttcttaacatggtttaata
                                                                                                                                                                                                                                                                                                459 cgaaggcgcctccttagccctttccatttcccctcggcggtgagtcagcgcgttaaagc
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scanning the human genome
Proc. Matl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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/db_xref="texon:9606"
-/clone="Plate=652 Col=21 Row=A"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 t
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Location/Qualifiers
1. 436
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AQ405681.1 GI:4415669
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RESULT 9 AQ405681/c DEFINITION

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Gaps

0;

Indels

BASE COUNT ORIGIN

FEATURES

Length 650;

numan.

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 11 AW351850/c

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DEFINITION

LOCUS

ACCESSION

VERSION

Brazil

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Colone_lib="HT0619"

/dev_stage="Adult"
/dev_stage=
                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 222)
1 (bases 2 to 222)
1 (bases 3 to 222)
1 (bases 3 to 222)
1 (bases 4 to 222)
1 (bases 6 to 222)
1 (bases 6 to 222)
1 (bases 7 to 222)
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Fax: +55-11-2707001
Fax: +
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1 (bases 1 to 393)
Akopyants,N.S., Clifton,S.W., Martin,J., Pape,D., Wylie,T., Li,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Liaboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ851405 393 bp DNA GSS 13-APR-2001 LMAJFV1_lm40b11.yl Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm40b11 5', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .222
/organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence start: 60
High quality sequence stop: 91.
Location/Qualifiers
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Leishmania major
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AQ851405
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/organism="Homo saplens"
/db.xef="texon:9606"
/clone_lib="CT0199"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0199-
180999-012-A09&t3=1999-09-18&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                               AW351850 166 bp mRNA EST 01-FEB-2000 RC1-CT0199-180999-012-A09 CT0199 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 5.0%; Score 35.6; D Similarity 58.5%; Pred. No. 3.3; 62; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 51
High quality sequence stop: 166.
Location/Qualifiers
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AW351850.1 GI:6849563
481 tecattteeceteggegg 499
                                                    248 TCCACCGACACCTTGGCAG 266
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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AUTHORS

nemnt EST

BF352878 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS' SOURCE

RESULT 12

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Query Match

Matches

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BASE COUNT ORIGIN

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/clone_lib="683 - 14 day immature embryo from Hake lab (HS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ253065 494 bp DNA GSS 15-JUN-2000
RPCI-23-94All.TV RPCI-23 Mus musculus genomic clone RPCI-23-94All,
                Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 taaaagactggccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgac 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Express); Site_1: XhOI; Site_2: EcoRI; Directionally cloned, 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."

97 c 154 g 116 t
                                                                                                                                             Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev_stage="14 days after pollination"
/lab_host="DH10B"
                                                                                                                                                                                                                      Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tael: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.6; DB pred. No. 4.4; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/cultivar="B73"
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AZ253065.1 GI:8566268
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ilarity 51.9%;
Conservative
                                                                                            (bases 1 to 492)
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Unpublished (1999)
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Matches 80; Conserv
                                                                                                            Walbot, V.
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VERSION
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                                                                                            REFERENCE
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Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Glbbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by Shotgun sequencing: a resource for DNA Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)

A contact: Akopyants, NS / Beverley, SM Mashigton University School of Medicine Mashigton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

DNA Sequencing by: Mashington University Genome Sequencing Center If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For information no betaining clone material please contact: Natalia S. Akopyants Ph.D.
University Genome Sequencing Center For information no obtaining clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: Shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Friedlin Strain VI"
/db_xref="taxon:564"
/db_xref="Laxon:564"
/clone="LMATVI_LIN40bl1"
/clone_lib="Leishmania major FVI random genomic library"
/lab_host="ToPl0 (Invitrogen)"
/lab_host="ToPl0 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's EcoRV site."
55 a 97 c 116 g 75 t
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683016G08.x1 683 - 14 day immature embryo from Hake lab (HS) Zea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GTCCGTAGCGGCAGTGCTGCGAGAACCTCACCCTCAAGCAGCGCCAGTTGCTGGTGCGGGT 244
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Location/Qualifiers
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Matches 74; Conservative
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Gaps

15-JUN-2000

Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research

Unpublished (1999) Other_GSSs: RPCI-23-94A11.TJ

JOURNAL COMMENT

TITLE

mays cDNA, mRNA sequence.

GI:6022249

AW067177.1 Zea mays. Zea mays

EST.

KEYWORDS SOURCE

ORGANISM

AW067177

ACCESSION VERSION

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CooRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHOB electrocompetent cells (BRL Life Technologies).

71 c 73 g 130 t
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                                                                                                                              library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea of Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Seq primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 cgcttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 gcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagt 360
                                                                          Email: szhaoetigr.org
Clones are derived from the mouse BAC_library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 CTCTAAAACATTTTTTTAAAAAAGTCTATTTCCCCAAATGAAGATGATAAATCCACCT 377
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Pred. No. 4.4;
0; Mismatches 84; Indels 0;
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9712 Medical Center Dr., Rockville, MD 20850, USA
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Job time: 12059 sec
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/clone="RPCI-23-94A11"
/clone_lib="RPCI-23"
/sex="Female"
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1. .494
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Matches 86; Conservative
                            Tel: 301 838
Fax: 301 838
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/*tag= c
/label= orf3
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/label= LysG
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ID AAT96816 standard; DNA; 2374
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/label= LysE
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                             - nucleic search, using sw model
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WB. This sequence has been created from the information given in table 2
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                                                                                                                                                                                                                                                                 This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulaton
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                                                                                                                   by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium
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Pred. No. 2.6e-223;
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 (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
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Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:53.
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                   gcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctggacgcctt
                                                                                                  gctgaaatcccgttaaccatcgccatcaacgcagattcgctatccacatgg
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99DE-1030476.
99US-0142101.
99DE-1031415.
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99DE-1032928.
99DE-1033004.
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99DE-1033006.
99US-0148613.
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99DE-1032126
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Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:49
                                                                                                                                                                                                                                                     fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; putine base; pyrimidine base; uncleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                                                                                       Corynebacterium glutamicum; metabolic pathway protein; MP protein;
          361 acttaagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaa
                                                                                                                                        BP.
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99DE-1031419.
99DE-1031420.
99DE-1031424.
99DE-1031424.
99DE-1031434.
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99DE-1031453.
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99DE-1031478.
99DE-1031510.
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99DE-1030476.
99US-0142101.
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99DE-1040764
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                                                 ctggacactttgctc 435
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                                                                                                                                                                                                                                                                                 Haberhauer
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                                                                                                                                                                                                                                                                                 Zelder
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                                   99DE-1040832.
99DE-1041378.
99DE-1041379.
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99DE-1041394.
99DE-1041396.
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99DE-1042095
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Best Local Similarity 100.
Matches 435; Conservative
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                                                                                                                                                                                                                                                                               Pompejus M, Kroeger
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                      27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
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31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
03-SEP-1999;
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Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                 delta 2; virulence; avirulence; attenuation; gene deletion; bbacteria; vaccine; infection; marker; ss.
Location/Qualifiers
3382.14071
7*tag= "BCG delta 1 deletion region"
                                                                                                                                                       BCG deletion region 2 and flanking sequences
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                                                                          AAT33536 standard; DNA; 15239
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                                                                                                                              (first entry)
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Matches 166; Conserv
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Pred. No. 3.1e-123;
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100.0%; Pred. No. 3...
... 0; Mismatches
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                                                           99DE-1041380
99DE-1041394.
99DE-1041396.
99DE-1042076.
          99DE-1040766
                                    99DE-1041378
99DE-1041379
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99DE-1042086
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99DE-1042088
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Best Local Similarity 100.
Matches 406; Conservative
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                                                                                                                                                                                                                                                                                                WPI; 2001-137957/14.
P-PSDB; AAB79658.
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                                    31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 477
                                                                          This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta2. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT33537) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the deletion; the deletions are detected either by detecting the presence or absense of deletion junctions (see AAT33538-46), or by detecting the presence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of
                                                                                                                                                                                                                                                                                                                                                                        The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 15239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15239 BP; 2878 A; 4791 C; 4729 G; 2841 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 63.2; DB 17;
55.3%; Pred. No. 7.4e-10;
iive 0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunological assays and in vaccines
Example 1; Fig 2; 66pp; English.
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Genomic library; bacteria; human upper airway; otitis media; sinusitis;
                                                             atgagiccitcgcgcttaaticcitgittaaicaccagiacaitcigcggiccgaiggac 288
tecacettgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                   170 CCAAAAATCCCGGCGAAATCAGGACCAAATCGCTGATAGCACAAAGTAAGGCAATCATA 111
               atgccacccagcgcataatatcgagcacgatcggcggcggcattggacaaaagatcaacg
                                                                                              cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca
                                                                                                                                                         289 agtaaaagactggccccaaaagcagacctgtaatgaa 326
                                                                                                                                                                                                       bronchopulmonary; endocarditis; meningitis; ss
                                                                                                                                                                                                                                                                           AAF28535 standard; DNA; 45613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6-JUN-2000; 2000WO-US16649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                             Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1999;
                                                                                                                                                                                                                                                                                                                          04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lagace RE,
                                                                                                                                                                                                                                                                                                   AAF28535;
                                                                                                                                                                                                                                                               AAF28535/c
 49
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                                                                                                                                                                                                                                                                                                   The present sequence is the yggA gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increase accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of L-amino acids by an Escherichia bacterium increasing the expression amount of an L-amino acid excretion
5313 ctacatgtcacccctcggctgtcagtcagcgcatcaagtcgttggagcagcagtcggc 5372
                                              caggtgctggtggtcagggaaaagccatgtcgggcgacgacgcaggtatcccgctgttg 5432
                                                                                 gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakanishi K, Aleshin VV, Troshin PV;
                                                                                                                                                                                                                                                                                               E.\ coli; yggA gene; amino acid production; excretion protein gene; amino acid excretion protein; ds.
                                                                      caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                       cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 636 BP; 120 A; 143 C; 180 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 24; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "YggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The bacterium used is E. coli.
                                                                                                                                                                                        AAA52691/c
ID AAA52691 standard; DNA; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-0125263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98RU-0124016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99RU-0104431
                                                                                                                                                                                                                                                                          Escherichia coli yggA gene.
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-414802/36.
P-PSDB; AAB01789.
                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Livshits VA,
Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                         EP1016710-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1998;
09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises
protein -
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                         Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 45613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.4; DB 22;
Pred. No. 0.00098;
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 180-191; 545pp; English.
ΚL;
Berg
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Patterson C,
                                                                            WPI; 2001-041427/05.
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Best Local Similarity
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Gaps

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Length 636; Indels

Score 60.4; DB 21; Pred. No. 1e-09; 0; Mismatches 136;

8.5%; 51.1%;

Query Match
Best Local Similarity 51.13
Matches 142; Conservative

486 ttccccctcggcggtgagtcagcgcttaaagctctcgagcatcacgtgggtcgagtgt

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1461 CACTCTTGCTGTTGTTGCTGAGGAGGATCTCTCGACGGTGCAGCGCATGAACTCCGCAT 1402
                                                     1401 TACTCCCTCCGCTGTGAGCCAGCGGCTCAAGGCTTTGGAGACTCTTCTTGGTCAGGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 or more contiguous nucleotides identical to sequence previously ledentified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the previous of the method is also used to evaluate agents for their
                                                                             Inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                                  10609 ATGAATACCACAAATCTTGCCACTTTTGTTGCAGTTATGCAGACAGGCAGCATCTCTAGT 10550
                        406 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 465
  Gaps
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.4%; Score 45.2; DB 20; Length Best Local Similarity 51.0%; Pred. No. 0.00032; Matches 107; Conservative 0; Mismatches 103; Indels
 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4915 BP; 967 A; 1521 C; 1591 G; 828 T; 8 other;
                                                                                                                                                                                                                                                                                                                                   Stealth virus; detection; diagnosis; infection;
                                                                                                                                                                                                                                                                                                          Stealth virus nucleic acid clone, SEQ ID NO: 9.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Page 40-42; 95pp; English.
                                                                                                                                                           10489 GATGAATTTGGGACGGCGTTGTT 10467
                                                                                                                                  catcacgtgggtcgagtgttggt 548
 .;
0
                                                                                                                                                                                                                            AAX84317 standard; DNA; 4915 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strains of stealth virus
                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US27744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0001184
                                                                                                                                                                                                                                                                                (first entry)
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MART/) MARTIN
                                                                                                                                                                                                                                                                                                                                                            Stealth virus
                                                                                                                                                                                                                                                                                                                                                                                     WO9934019-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1997;
                                                                                                                                                                                                                                                                                08-SEP-1999
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82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determine
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 Matches
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AAX84317/
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1341 ATTGGTGCGCTCAAAGCCAGTGCGTCTGACGACACCGGGGGCGTCCATCGTTCGGTTTGC 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            group, useful as labels in allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 ttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactggcc 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 ggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.8; DB red. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.034
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                      1281 TCGTCAGACCGAGATGCTCGAGAGGGAGAC 1252
                                                                                                   606 geggaaaatggtgttgetgeaageagaaae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                    AAF58252 standard; DNA; 936 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2000; 2000WO-US20476
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17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single surface
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                                                                                                                                                                                                                                                                                                                                  AAF58252;
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                                                                                                                                                                                                                                                            AAF58252
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                       483
                                                                                                   364 taagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaactg 423
                                                                                                                                                                                                       811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 atgaacaaaaagacgtcagaaattaaacacacgagaagaagcgcaatgagtccttcgcgc 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                            304 cccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagtact
                                                                     424 gacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctttcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 5.3%; Score 37.8; DB 22; Local Similarity 5.8%; Pred. No. 0.034; es 18; Conservative 163; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                            AAF58257 standard; DNA; 936 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide D1954
                                                                                                                                                                                                                                        484 atttcccctc 494
                                                                                                                                                                                                                                                                          812 ccccccccc 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1999;
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Best Local S
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                                                                                                                                                                                                                                                                                                                            RESULT 10
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                                                                                                                                                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
 cccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagtact 363
                                                                   taagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaactg 423
                                                                                       184 atgaacaaaaagacgtcagaaattaaacacacgagaagaaccgcaatgagtccttcgcgc 243
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                                 gacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctttcc
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5.8%; Pred. No. 0.034;
Ive 163; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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                                                                                                                                                                                                                                                                                                                        AAF58254 standard; DNA; 936 BP
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17-MAR-2000; 2000US-0190259.
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nes 18; Conserv
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                                                 Electron-transfer group; ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259
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 ttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactggcc 303
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                                                                       taagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaactg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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17-MAR-2000; 2000US-0190259
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812 cccccccc 822
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936 BP

(first entry)

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.3%; Score 37.8; DB 22; Best Local Similarity 5.8%; Pred. No. 0.034; Matches 18; Conservative 163; Mismatches 130;
                                                                                                                                                                                                                                          Example 6; Page 128; 159pp; English
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WPI; 2001-159728/16.
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                                 184 atgaacaaaaagacgtcagaaattaaacacacgagaagaaccgcaatgagtccttcgcgc 243
                                                                                                         244 ttaatteettgtttaateaecagtaeattetgeggteegatggaeagtaaaagaetggee 303
                                                                                                                                                                              304 cccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagtact 363
                                                                                                                                                                                                                                                   taagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaactg 423
                                                                                                                                                                                                                                                                                     Sequence of BamHI/Sall fragment of the tfdA gene which encodes 2,4-dichlorophenoxyacetic acid (2,4-D) mono-oxygenase.
                                                                                                                                                                                                   The tfdA gene product is a 2,4-D decomposing protein. A.eutrophus JMP 134 contains an 80 kb plasmid, pJP4, which carries the genes coding for 2,4-D decomposition. Plasmids and bacteria contg. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmids and bacteria contg. gene tfdA for 2,4\text{-}D\text{-}mono:oxygenase} isolated using new Alcaligenes eutrophus transposon mutants
18; Conservative 163; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicide resistance; halogenated aromatic cpd; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "DNA SQ claimed"
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748..1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCHD ) SCHERING AG. (STRE/) STREBER W.R. (MACQ-) MACQUARIE UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streber W, Timmis KN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      812 ccccccccc 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mono-oxygenase; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
 atgaacaaaaagacgtcagaaattaaacacacgagaagaagcaccgcaatgagtccttcgcgc 243
                                                                     ttaatteettgtttaateaceagtaeattetgeggteegatggaeagtaaaagaetggee 303
                                                                                                                                            cccaaaagcagacetgtaatgaagatttccatgatcaccatcgtgacctatggaagtact 363
                                                                                                                                                                                                                  taagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaactg 423
                                                                                                                                                                                                                                                                                                            Nucleic acids containing electron-transfer group, useful as labels in
                                 gacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctttcc 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 938;
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17-MAR-2000; 2000US-0190259.
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Best Local Similarity
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RESULT 13

AAF58255

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gene are useful for prodn. of 2,4-D mono-oxygenase and for transferring the ability to decompose 2,4-D to other micro-organisms (which could then be useful for cleaning waste water polluted by halogenated aromatic cpds.) or to plants (to impart tolerance to 2,4-
                                                                                                                                                                                               418 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 477
                                                                                                                                                                                                                478 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 537
                                                                                                                                                                                                                                                                          Using presence of tfdA gene to select transgenic plants - imparting resistance to 2,4-di:chloro:phenoxy:acetic acid, esp. sweetgum (Liquidamber) trees contg. this gene and plantations of them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plant; tfdA gene; 2,4-dichlorophenoxyacetic acid; 2,4-D; herbicide resistance; sweetgum; Liquidamber styraciflua; hardwood; plantation; crop improvement; selectable marker; pUCW200; vector;
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                                                                                                                                   Score 37; DB 9; Length 2058; Pred. No. 0.098;
                                                                                                                                                                  65; Indels
                                                                                         Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                                                                                                                                                                  0; Mismatches
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751..1611
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ97857 standard; DNA; 2058 BP
                                                                                                                                                                                                                                                                                                                 538 cgagtgttggtatcgcgcacc 558
                                                                                                                                                                                                                                                                                                                                                410 GIGITGITGITCGAGCGCAGC 390
                                                                                                                                     Query Match 5.2%;
Best Local Similarity 53.9%;
Matches 76; Conservative
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94US-0179667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P. aeruginosa tfdA gene
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P-PSDB; AAR79659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-1994;
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                                                                                                                                                                           allowing selection of transgenic plants and reducing the cost of site prepn. and maintenance.
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0
                                                                                           Score 37; DB 16; Length 2058;
Pred. No. 0.098;
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                                             Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
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ŏ	GenCore version 4.5	12	184	16.9	312	22	AAB79618 AAB80067	
Copyright (c) 1993 -) 1993 - 2000 Compugen Ltd.	14	180.5	16.5	315	22	AAB76845	
		15	180.5	16.5	316	21	AAG35251	
		16	180.5	16.5	371	21	AAG35250	
OM protein - protein search, using sw model	sing sw model	17	180.5	16.5	388	21	AAG35249	
		18	175	16.0	333	18	AAW19736	
Run on: September 13,	September 13, 2001, 17:33:09; Search time 34.57 Seconds	19	175	16.0	333	20	AAW99386	
	(without	20	166.5	15.3	316	21	AAG39500	
	378.790 Million cell updates/sec	21	166.5	15.3	324	21	AAG39499	
		22	166.5	.15.3	365	21	AAG39498	
Title: US-09-105-117I-2	[-2	23	164	15.0	192	21	AAG09267	
core:		24	163.5	15.0	357	21	AAG41676	
Sequence: 1 DTPLEETMYALRDIVASGKA	RDIVASGKASHDAGINIWAKATDSKTREN 216	25	163.5	15.0	375	21	AAG52050	
		26	163.5	15.0	377	21	AAG52049	
Scoring table: BLOSUM62		27	163.5	15.0	386	21	AAG52048	
Gapop 10.0 , Gapext 0	Japext 0.5	28	163.5	15.0	389	21	AAG52008	
		53	163.5	15.0	412	21	AAG41675	
Searched: 412676 seqs, 60623988	50623988 residues	30	163.5	15.0	419	21	AAG41674	
		31	162.5	14.9	331	50	AAY49837	
Total number of hits satisfying chosen	chosen parameters: 412676 .	32	162.5	14.9	331	50	AAY24920	
		33	162.5	14.9	331	21	AAB09902	
Minimum DB seq length: 0		34	162	14.8	340	21	AAG38206	
Maximum DB seq length: 2000000000	000	35	162	14.8	349	21	AAG38205	
		36	162	14.8	351	21	AAG38204	
Post-processing: Minimum Match 0%		37	160.5	14.7	181	21	AAG37809	
Maximum Match	100%	38	160.5	14.7	331	50	AAW93088	
Listing first 45 summaries	45 summaries	39	159.5	14.6	330	50	AAW93086	
		40	158	14.5	329	19	AAW71534	
Database : A_Geneseq_0601:*	*:1	41	156.5	14.3	327	21	AAB09903	
1: /SIDS8/gcgć	/SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*	42	156.5	14.3	338	50	AAW93089	
2: /SIDS8/gcgd	/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*	43	156.5	14.3	338	20	AAW93090	
3: /SIDS8/gcgd	/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*	44	154.5		278	21	AAG36393	
4: /SIDS8/gcgc	SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*	45	154.5	14.2	286	21	AAG36392	

Corynebacterium gl Corynebacterium gl Zea mays protein f Zea mays protein f Zea mays protein f Zea mays protein f Sugar blosynthesis S.crythraea dTDP-4 Arabidopsis thalia Human aflatoxin Bl Human aflatoxin Bl

Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human CPRM3 protei

Arabidopsis thalia

protei protei

Human CPRM1

Helicobacter polyp Rat aflatoxin Bl a

Mouse mCPRM1 allel Mouse mCPRM1 allel Arabidopsis thalia Arabidopsis thalia

ALIGNMENTS

A_Geneseq_0601:*

| SIDS8/gcddata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcddata/geneseq/geneseqp/AA1981.DAT:*
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| SIDS8/gcddata/geneseqp/Geneseqp/AA1991.DAT:*
| SIDS8/gcgdata/geneseqp/geneseqp/AA1991.DAT:*

LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive. Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH AAW37716 standard; Protein; 216 AA Σ 95DE-1048222 95DE-1048222 glutamicum orf3 protein Corynebacterium glutamicum (first entry) Sahm H, WPI; 1997-333867/31. N-PSDB; AAT96816 DE19548222-A1 22-DEC-1995; 22-DEC-1995; 12-MAR-1998 26-JUN-1997. Eggeling L, AAW37716; Н AAW37716 RESULT

> C. glutamicum orf3
> Corynebacterium gl Corynebacterium gl Corynebacterium gl Corynerium gl Corynerium gl Corynerium glaker-like potass Shaker-like potass Sea mays protein f Zea mays protein f Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES AAW37716 AAB76844 AAY52837 AAG35919 AAG09266 AAG39051 AAG39050 AAG39049 AAW23389 AAG35920 AAW23388 221 221 221 221 221 221 221 DB 290 348 329 329 329 266 216 216 328 Length Query 100.0 Score 1091 792 225 205 202 195.5 195.5 195.1 195.1

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09-JUL-1999;
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                           This sequence is the Orf3 protein product, involved in lysine production. Ly65 and Ly8E encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microoraganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
                                                                                                                                                                                                                                                                    61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                 NNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSL 180
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                                                                                                                                                                                                                 1 DIPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW
                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
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0
                                                                                                                                                                         Length 216;
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                                                                                                                                                                         DB 18;
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Pred. No. 1.3e-102;
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0
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                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1091; Best Local Similarity 100.0%; Pred. No. 1.3 Matches 216; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome mapping; genetic engineering
         Disclosure; Page 9; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                             AAB76844 standard; Protein; 290
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99DE-1032125
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99DE-1031478
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99DE-1032180
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99DE-1032190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                           216 AA;
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in ABB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV
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-haq 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 1109; 1119pp; English.
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99DE-1032212.
99DE-1032227.
99DE-1032228.
                                                            99DE-1032229.
99DE-1032230.
99DE-1032927.
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Best Local Similarity 99.4%;
Matches 156; Conservative
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09-JUL-1999;
14-JUL-1999;
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ID AAY5
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Isoprenoid; microorganism; detection; antibacterial; herbicide; heart disease; osteoporosis; haemostasis; cancer; immunopotentiation; health food; antifouling coating; farnesyl pyrolinic acid; pyruvic acid; 1-deoxy-D-xylulose-5-phosphate; glycerylaldehyde-3-phosphate; 2-C-methyl-D-erythreitol-4-phosphate.
                                                                                                                                                                                                                                                                                                 Preparation of recombinant isoprenoid compounds useful for treatme heart diseases, osteoporosis and hemostatis, preventing cancer and
                                                                                                                                                                                                                                             Hashimoto S, Motoyama H, Ozaki A,
                                           coli protein sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 70-72; 145pp; Japanese.
                                                                                                                                                                                      98JP-0103101.
98JP-0221910.
99JP-0035739.
                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                      99WO-JP01987
                         26-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                    immunopotentiation
                                                                                                                  Escherichia coli.
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                                                                                                                                   W09953071-A1
                                                                                                                                                                     14-APR-1999;
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05-AUG-1998;
                                                                                                                                                                                                         15-FEB-1999;
                                           Sscherichia
                                                                                                                                                    21-0CT-1999
                                                                                                                                                                                                                                             Miyake K,
Takahashi 9
       AAY52837;
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treatment of

Kuzuyama T;

Seto H,

The present invention describes the preparation of an isoprenoid compound comprising at least 1 DNA e.g. encoding proteins which elevate the efficiency of the synthesis or DNA encoding a farnesyl pyrolinic producing enzyme. The method of preparation of an isoprenoid compound comprises using at least 1 DNA, a vector, cloned cells, their derivative recombinant DNAs or transformed products in a culture system and extracting the isoprenoid accumulated in the medium. The DNA encodes at least 1 of the following: (a) a compound for activating or catalysing the production of 1-deoxy-b-xylulose-5-phosphate from pyruvic acid and glycerylalehyde-3-phosphate; (b) an enzyme producing farnesyl pyrolinic acid; (c) a protein which elevates the efficiency of synthesis of isoprenoid compounds and comprises a 3 or 4 amino acid sequence optionally with 1 or more of the amino acids being deleted or substituted or an additional amino acid being inserted; (d) a protein which activates or catalyses the production of 2-C-methyl-b-erythraticol-compound actalyses the production of 2-c-methyl-b-erythraticol-compound actalyses the production of 2-c-methyl-b-erythraticol-compound or reaction and is a string end or hybrid activates a target compound or reaction and is a string end or hybrid of the presenting coarings. The isoprenoids also inhibit enzymatic reactions antifouling coatings. The isoprenoids also inhibit enzymatic reactions of herbicides. The present sequence is used in the exemplification of the present invention.

348 AA; Sequence

9 63; Indels 26; Gaps DTPLEETWYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEGCPLLIH-QPSYSIINR 59 20.6%; Score 225; DB 20; Length 348; 31.9%; Pred. No. 1.6e-14; ive 39; Mismatches 63; Indels 20 Query Match
Best Local Similarity 31.9%,
Matches 60; Conservative Т

This polypeptide sequence Kv beta 1 consists of the core region of a beta-subunit of a Shaker-like potassium ion channel (SPC). This core region can bind to a polypeptide consisting of the N-terminal A and B box (NAB) domain and the NAB-S1 (the first transmembrane spanning domain linking region of the alpha-subunit of SPC. The polypeptides or the nucleic acid encoding them can be introduced into the cytoplasm of a cell to modulate the flow of potassium ions through a cytoplasmic cell 156 ntpieetlealndvvkagkaryigassmhasqfaqalelqkqhgwaqfvsmqdhynliyr 215 Shaker-like potassium ion channel beta-subunit core region Kv beta 1. Polypeptide(s) derived from Shaker-like potassium ion channel alpha and beta subunits - used to alter potassium ion levels in a cell, e.g. for treating neurological disorders, tumours, metabolic disease Shaker-like potassium ion channel; SPC: beta subunit; core region; Kv beta 1; N-terminal A and B box; NAB; treatment; cardiac disease; tumour; auto immune disease. WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ-----GKSL 114 SEGMLNVNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQL -----eeeremlplcyqegvavipwsplargrltr-----pwgettarlvsdevgknl (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE Claim 15; Pages 51-52; 106pp; English. AAW23388 standard; protein; 329 AA. 97WO-US02292. 96US-0606143. (first entry) WPI; 1997-435164/40. e.g. for treating ne and cardiac disease 174 DNSLDSLN 181 dellnavd 324 WO9731112-A2. 18-FEB-1997; 23-FEB-1996; 02-APR-1998 28-AUG-1997 AAW23388; Mammalia. Li M; 9 317 AAW23388 ò 셤 ŏ Pp ò

membrane. Potcassium in channels regulate the action potentials, cardiac pacemaking and neurotransmitter release in excitable tissues. In non-excitable tissues they play important roles in hormone secretion, cell proliferation, cell volume regulation and lymphocyte differentiation. Molecules which bind to the alpha or beta-subunit polypeptides can be detected by contacting the polypeptides, with a putative NAB and NAB-51 linking region of an alpha-subunit or with a putative core region of a beta-subunit respectively, and determining whether or not binding occurs. These polypeptides and the encoding disorders, e.g. neurological disorders, tumours, metabolic diseases, cardiac disease and autoimmune disease,

329 AA; Sequence 9

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99US-0132485
99US-0132486
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Best Local Similarity
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06-MAY-1999;
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                                                                                                                                                185 ekve----vqlpelyhkigvgamtwsplacgiisgkygngvpessraslkcygwlkeri 239
                                                                                                                                                                                          125 ntpmeeivramthvinggmamywgtsrwsameimeaysvargfnmippvcegaeyhlfgr 184
                                                                                                                       60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG--KSLSEGM 117
                                                                                                                                                                         118 LNVNNIDMVRKLND---IAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLD 174
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                                                                                                                                                                                                                                                                                                                                                                                                                 beta subunit; core region;
treatment; cardiac disease;
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                                                                     1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAE-EGCPLLIHQPSYSIINR
                                                18;
                      Length 329;
                                                Indels
                                                83;
                      Score 205; DB 18;
Pred. No. 1.5e-12;
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                                               39; Mismatches
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Kv beta 2; N-terminal A and B box;
tumour; auto immune disease.
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Best Local Similarity 31.0%
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and cardiac disease
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEG-CPLLIHQPSYSIINR 59
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Pred. No. 3.1e-12;
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64; Conservative 3
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22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 26-JHL-1999;	27 - JUL - 1999; 27 - JUL - 1999;	27-JUL-1999; 28-JUL-1999;	02-AUG-1999; 02-AUG-1999;	02-AUG-1999;	03-AUG-1999; 04-AUG-1999;	04-AUG-1999;	05-AUG-1999;	06-AUG-1999;	09-AUG-1999;	09-AUG-1999;	11-AUG-1999;	12-AUG-1999;	13-AUG-1999; 13-AUG-1999;	16-AUG-1999;	17-AUG-1999; 18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	20-AUG-1999; 23-AUG-1999;		25-AUG-1999;	27 - AUG-1999;	27-AUG-1999;	27-AUG-1999; 30-AUG-1999;	31-AUG-1999;	01-SEP-1999; 07-SEP-1999;	10-SEP-1999;	13-SEP-1999; 15-SEP-1999;	16-SEP-1999;	20-SEP-1999; 22-SEP-1999;	23-SEP-1999;	24-SEP-1999; 28-SEP-1999;	29-SEP-1999;	04-0CT-1999; 05-0CT-1999;						14-0CT-1999;	14-OCT-1999;	14-0CT-1999; 14-0CT-1999;	14-OCT-1999;	18-OCT-1999; 21-OCT-1999;	21-0CT-1999;	21-OCT-1999;	21-0CT-1999;
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07 - MAY - 1999;
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                                                                                                                            Query Match 17.9%; Score 195.5; DB 21; Length Best Local Similarity 30.1%; Pred. No. 1e-11; Matches 65; Conservative 39; Mismatches 89; Indels
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99US-0160815.
99US-0160980.
99US-0160981.
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iive 39; Mismatches 89
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein;
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fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes.
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                                                                                                          04-JAN-2001
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in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                        59 RWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR-ASQGKSLS-EG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TPLEETMYALRDIVASGKALYVGISSYGP---ELTAEAAEFMAEEGCPLLIHQPSYSIIN 58
                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum MP protein sequence SEQ ID NO:868.
                                                                                                                                                                                               Length 312;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                               16.9%; Score 184; DB 22; 29.9%; Pred. No. 1.9e-10;
                                                                                                                                                                                                                                            34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB80067 standard; Protein; 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 LDSLNNLEFSDAELEAIDEIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 lka-esvtlptpitgalddvs 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990S-0142101.
99DE-1031415.
99DE-1031418.
99DE-1031419.
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99DE-1031428
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99DE-1031478
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99DE-1031592
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membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
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MLNVNNIDMYRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176
                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum MCT protein SEQ ID NO:672.
                                                                     238 yldnrgriivdaldtaakglgispavtattwvrdrpg
                                                                                                                                                                                                                                                                                                                                                                        genome mapping; genetic engineering
                                                                                                                                                                                                 AAB76845 standard; Protein; 315 AA.
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| lka-esvtlptpitqalddvs 311
                                                                                                   LDSLNNLEFSDAELEAIDEIS 197
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99DE-1040833.
99DE-1041378.
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99DE-1032190.
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99DE-1032227
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200100805-A2.
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                                                                                                                                                                                                                            AAB76845;
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              184
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                                                                                                                                                                                    AAB76845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purline and pyrimidine bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 tpphevadtldyavrtgrvryagvrgysgwqlavthaasnhaaasarpvvvaqneyslle 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%; Score 184; DB 22;
29.9%; Pred. No. 1.9e-10;
Live 34; Mismatches 89;
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                                       99DE-1032125.
99DE-1032126.
99DE-1032130.
99DE-1032186.
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99DE-1032926.
99DE-1032928.
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99DE-1033005.
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99US-0148613.
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99DE-1040765.
99DE-1040766.
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99DE-1041379.
99DE-1041380.
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99DE-1041396.
99DE-1042076.
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99DE-1032228
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99DE-1032230
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99DE-1042079
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99DE-1042087
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Best Local Similarity
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MP nuclet
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31-AUG-1999;
31-AUG-1999;
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-AUG-1999

(BADI) BASF AG.

59 RWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR-ASQGKSLS-EG 116

90;

Matches

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Sequence

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99US-0128234
99US-0128714
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99US-0134768
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99US-0132863
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                   16-APR-1999;
19-APR-1999;
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                                                                                                      23-APR-1999
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06-MAY-1
07-MAY-1
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  9
                                                                                                                                              AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. glutamicum or related bacteria, as reference points for mapping C. glutamicum or related bacteria, as reference points for mapping C. glutamicum, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                  Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                       64 PGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQ-GKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSL 180
                                                                                                                                                                                                                                                                                                                                                        4 LEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEE 63
                                                                                                                                                                                                                                                                                                                                                                                                                             189 -kdyeenvqplaekhgvavfpyfalaaglltgkytskedisgkaragqldryasdeafav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| :| | | | | : :||||:: | | ||: | | ||| | :: | 248 -----vtelravadelgvapttvalawlv-----ahgvtapiasvskvegl-kdlmav
            Haberhauer G;
                                                                                                                                                                                                                                                                                                            16.5%; Score 180.5; DB 22; Length 315; 29.4%; Pred. No. 4.4e-10;
                                                                                                                                                                                                                                                                                                                                     80; Indels
            Zelder O,
                                                                                                                                                                                                                                                                                                                                  38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays protein fragment SEQ ID NO: 43035.
                                                                                                                         Claim 20; Page 1111-1112; 1119pp; English.
            Schroeder H,
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99US-0123180.
99US-0123548.
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Best Local Similarity 29.49
Matches 58; Conservative
            Pompejus M, Kroeger B,
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                                WPI; 2001-071486/08.
N-PSDB; AAF68078.
                                                                                                                                                                                                                                                                           315 AA;
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05-MAR-1999;
09-MAR-1999;
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990S-0149368.
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99US-0153070.
99US-0153758.
99US-0154018.
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99US-0154779.
99US-0155139.
99US-0155486.
99US-0155659.
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99US-0157753.
99US-0157865.
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13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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10-SEP-1999
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30-AUG-1999
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61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKY-LDGIPEGSRASQGKSLSEGMLN 119
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9908-0158029
9908-0158232
9908-0159293
9908-0159294
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9908-0159329
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07-0cr-1999, 08-0cr-1999, 12-0cr-1999, 13-0cr-1999, 13-0cr-1999, 14-0cr-1999, 14-0cr-1999, 14-0cr-1999, 21-0cr-1999, 22-0cr-1999, 22-0cr-1999, 25-0cr-1999, 25-0cr-1999, 26-0cr-1999, 26-0c
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29-OCT-1999;
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023016 arabidopsis
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Q9rs66 deinococcus
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09pcq5 xylella fas
09hi90 thermoplasm
09x265 thermotoga
02x267 helianthus
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055493 synechocyst
09i0u9 pseudomonas
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"A new type of transporter with a new type of cellular function: L-
lysine export from Corynobacterium glutamicum.";

MOI. Microbiol. 22:815-826(1996).

EMBL: X96471; CAA65325.1;

SROUGENCE 209 AA; 22450 MW; 06549D44F0BC0100 CRC64;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
NCBI_TaxID=1718;
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Last annotation update)
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100.0%; Pred. No. 1.2e-75;
tive 0; Mismatches 0;
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Matches 209; Conserv
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- 2000 Compugen Ltd.
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Listing first 45 summaries
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Copyright (c) 1993
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Perfect score:
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CAB42946.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliver K.) Harris D.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        122 NIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSLN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                             EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNVN 121
                                                                                                                                                                                                                                                                                                                                                                  2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV 61
                                                                                                                Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL50223; CAG155.1;
EMBL; AL450223; CAG155.1;
SEQUENCE 348 AA; 38441 MW; CFF77941897D9C1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                      48.5%; Score 529; DB 2; Length 348; 54.3%; Pred. No. 6.2e-34; Live 29; Mismatches 54; Indels
 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) PUTATIVE ION CHANNEL SUBGNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 NLEFSDAELEAIDEIS-HDAGINIWAKA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                         SEQUENCE FROM N.A.
STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                           Matches 113; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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EMBL; U28377; AAA691681.; --
EMBL; AE000382; AAC76037.1; --
SEQUENCE 346 AA; 38832 MW; C70D4D43A3A57AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR----ASQGKSLSEG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomyces
                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeger K.J., Harris D.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.5%; Score 529.5; DB 2; 51.4%; Pred. No. 5.6e-34; Live 38; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::|||| || || || || ::| ::| 312 VQALNNLTFSTKELAQIDQHIADGELNLWQASSD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
181 AELEAIDEISHDAGINIWAKATDSKTREN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                  PRT;
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                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, PUTATIVE OXIDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 51.4%
Matches 110; Conservative
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                               ORF_0346.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
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Q9EWJ0 Q9EWJ0;

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242 DENIQKVRDLKSIADDLGVTRAQLALAWLLRQKG-----VSSVITGATKVNQIQDTVKA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 VINIDMVRKLINDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS 179
256 LTKERLEQVQALNDLAQSRGQSLAQMALAWVLRERDD-KVQGITSALIGASRPQQIIENV 314
                                                                                                                                                                                                                                                                                                                                             White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakazova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus. NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 AA; 35156 MW; B7614CCEE22A7104 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----
                                                                                                                                                                   ol-mar-2000 (TrEMBLrel. 13, Last sequence update) 01-Mar-2001 (TrEMBLrel. 16, Last annotation update) POTASSIUM CHANNEL, BETA SUBUNIT, PUTATIVE.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 283.5; DB 2 34.5%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                  Created)
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Bacteria; Thermotogales; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                  MEDLINE=20036896; PubMed=10567266;
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Pfam; PF00248; aldo_ket_red; 2.
Ionic channel.
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(TrEMBLrel. 12, I
(TrEMBLrel. 13, I
BETA SUBUNIT.
                               178 DSLNNLEFSDAELEAIDEI 196
                                               AALEHLKFTDEELIKIEKL 333
                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE002063; AAF11861.1;
TIGR; DR2317; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571-1577(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 LNNLEFSDAELEAIDEI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : || | |::|
296 A-GVRLSDDVQRRIEDI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                            Deinococcus radiodurans.
                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         radiodurans R1
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01-NOV-1999 (
01-MAY-2000 (
K+ CHANNEL, B
TM0313.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M.;
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Q9WYE9;
                                                                                                                                                   09RS10;
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Q9RS10
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                                                                                                                                                                EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR-ASQGKSLSEGMLNV 120
                                                                                                                                                                                 :||:|||| ||: : |||||||:::|
NTPIEETMGALKSALDSGKALYVGLSNYSAKET-EAAVLAAEKLGFKLLIHQPRYSMLDR 201
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                                                                                                      TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and nucleotide sequence of the beta-galactosidase gene from Lactococcus lactis ssp. lactis ATCC7962.";
Biotechnol. Lett. 19:179-183(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                          121 NNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSL
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Lee J.M., Chung D.K., Park J.H., Lee W.K., Chang H.C., Kim J.H.,
Lee H.J.;
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Lee H.J.;
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                                             Length 319;
                                                                         54; Indels
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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334 Aa; 37574 MW; 0DA15BAA867CE2A3 CRC64;
D0114179AE30038B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 37.6 KDA PROTEIN.
Lactococcus lactis.
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                                            Query Match 41.2%; Score 449; DB 2; Best Local Similarity 53.6%; Pred. No. 1.1e-27; Matches 105; Conservative 25; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                              334 AA
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Pfam; PF00248; aldo_ket_red; 1.
Hypothetical protein.
34702 MW;
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Best Local Similarity 50.8%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                    181 NNLEFSDAELEAIDEI 196
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301 GNLDFDADELARIDKI 316
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319
SEQUENCE
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255 SYLTEENFDVHDELDAVAGEVDATPAQTALAWLMHRDG------VTAPIVGARTVEQLTE 308
NRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQGKSLSE 115
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MEDLINE-2006483; PubMed-11016950;
Now W. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzall S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
"Genome sequence of Halobacterium species NRC-1.";
PPICO. NALL, Acad. Sci. U.S.A. 97:12176-12181(2000).
                                   201 DREIE--GD----YLEMIRSYGIAVCPWSPLGGGFLTGKYTREDGLTGESRAAESSRRFEE
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Halobacterium.
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EMBL: AE005035; AAC19415.1; -
Interpro: IPRO01395; -
SEQUENCE 336 Aa; 37376 MW; 04C7676CED9B8E04 CRC64;
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Matches 67; Conservative
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YAJO2 OR VNG0998G.
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SEQUENCE FROM N.A.
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                                                                                                            Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
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"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
TIGR; TM0313: -.
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U95374; AAB71807.1; -.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
0xiDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.5%; Score 267; DB 2; 33.8%; Pred. No. 2.4e-13; iive 43; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacterium volcanii (Haloferax volcanii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 EQLEENLKAVEIKEKLTEDVMEETEKILNE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQLDNSLDSLNNLE-FSDAELEAIDEISHD 199
                                                            STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001395; -.
PRINTS; PR00069; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 33.8% les 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.6% Best Local Similarity 32.1% Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pHV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ionic channel
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SEQUENCE
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Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO23590; CAA19066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 AA; 38430 MW; A57A25E60B05CAE9 CRC64;
                                                                                                   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
Schizosaccharomyces.
                                                                 Schizosaccharomyces pombe (Fission yeast).
   PUTATIVE POTASSIUM CHANNEL SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 32.89
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radiobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium rad
Plasmid pTi15955
                                                                                                                                                                                                   NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                   STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ionic channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOCA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Q44328;
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                                                                                                                                                                                                                                                                                                                                               Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Bala G.S., Baptista C.S., Barros M.H., Bonaccorsis E.D., Bordin S., Bove J.M., Eliones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Coutinho L.L., Cristoffani M., Dias-Neto E., Docena C., El-Dorry H., Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Racincani A.P., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Raga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Raga J.S., Franca E.E., Laigret F., Lopes S.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Mandon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Mandon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Mandon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Mandon J.B., Pereira B.K.C., Palmieri D.A., Paris A., Ade Soluza A.D.M., Ade Soluza A.B., Roberto P.G., Santelli R.V., Savasaki H.E., Ade Soluza A.P., Terenzi M.F., Truffi D., Tsai S.N., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., The Genome sequence of the plant pathogen Xylella fastidiosa."; Matsurero, IPROBLY PRESINTAL.

Mature 406:181-1992(2000).

Mature 406:181-1992(2000).

Mature 406:181-1992(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRA-----SQGKS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 LSEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINR 59
                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update) VOLTAGE-GATED POTASSIUM CHANNEL BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 AA.
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                                                                                                                                                                                                                                                                                                                              MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00069; ALDKETRDIASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 AA; 42793 MW;
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(TrEMBLrel. 07, I
(TrEMBLrel. 13, I
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Best Local Similarity 55.,
Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 LKENLRALQVVAALDA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                               xylella fastidiosa
                                                                                                                                                                                            NCBI_TaxID=2371;
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01-AUG-1998 (
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                   STRAIN-9A5C
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"Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the Tregion genes responsible for synthesis of this opine by the plant tumor.";
                                                                                                                                                                                                               61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
                                                     Gaps
                                                                                                                                                            144 PMEEVVRAFTQLIQDGKAFYWGTSEWS-AFEIEHAHHIATKYNLIAPVADQPQYNYLTRD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                   3 PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL--LIHQPSYSIINRW
                                                                                                                                                                                                                                                                  203 HFE-----KDLLPLQQIYGYGATVWSPLKSGILTGKYNDGIPEGSRLSTTFTSLAGQLQT
                                                                                                                                                                                                                                                                                                                     ----NNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                     Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA; 38846 MW; 21D4074605E80EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
20.9%; Score 227.5; DB 3; 32.8%; Pred. No. 3.5e-10; iive 37; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.5%; Score 213; DB 2; 32.5%; Pred. No. 5.1e-09; iive 35; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 178:3275-3284(1996).
EMBL; AF242881; AAB07785.1; -.
InterPro; IPR001395; -.
Pfam; PF00248; aldo_ket_red; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            177 LDSLNNLEFSD----AELEAIDEI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 VENVKAVEFIDKLTPEILKKIDEI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=15955;
MEDLINE=96236046; PubMed=8655509;
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Q9F2Z5
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  RESULT 14
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                                                  186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Bathman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Relzer J., Saier M.H., Hanocok R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an
2 TPLEETMYALRDIVASGKALYVGISSY------GPELTAEAAEFMAEEGCPLLIHQP
                             53 SYSIINRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQG
                                                                                                                            111 KSL----SEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALI
                                                                                                                                                                                                                                                    240 WTEPPVRDEERLWNI-----VDTLLSVADGRGVSAAQVALAWLI-----GRKAVTSIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
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Last annotation update)
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Best Local Similarity 33.0%; Pred. No. 7e-09;
Matches 66; Conservative 33; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 AA
                                                                                                                                                                                                                                                                                                                                      289 GGRTEAQFKDNL-AAADLQLSAEERKRLDDVS 319
                                                                                                                                                                                                                                                                                                      GASSVEQLDNSLDSLNNLEFSDAELEAIDEIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PAO1;
MEDLINE-20437337; Pubmed-10984043;
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PRINTS; PR00069; ALDKETRDTASE.
ProDom; PD002680; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL, AE004057, AAG07822.1;
InterPro; IPR001395;
InterPro; IPR001692;
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V-DLRLDEEVLAGIDAIHRE 339
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01-MAR-2001 (TrEMBLrel. 16,
PROBABLE OXIDOREDUCTASE.
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinsshi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL392149; CAC08308.1;
EXQUENCE 330 AA; 36116 MW; 5733CFEF9F7BEEA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TPFEEIWQAIDVLVQQGKILYAGSSNFPGYKIAQANEIAARRGGTIGLVSEQCLYNLAER 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEG--CPLLIHQPSYSIINR 59
                                                                                                                                    Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 RAE-----MEVIPAARDYGLGVIPWSPLHGGLLGGVIKKEATQGRRAS-GRA-ADALKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 330;
                                                                                                                                                                                                                                                                                                                                                                              Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels
                                                                                                                                                                                                                                                                              Seeger K.J., Harris D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                        Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 7.2e-09;
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32.0%; Pred. No. /...
''ve 36; Mismatches
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                                       Created)
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L-ELELSEELLTSLDEI 317
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PRELIMINARY;
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                                                                                              PUTATIVE OXIDOREDUCTASE. SCD19.07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
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SEQUENCÈ FROM N.A.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                     01-MAR-2001
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL138852; CAB72221.1;
InterPro; IPR001395;
InterPro; IPR00069; AlDKETRDASE.
SEQUENCE 336 AA; 37060 MW; C68A60A31C9BB62C CRC64;
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                                                                                                                                                                                                STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Brown S.P., Harris D.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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OM protein - protein search, using sw model

September 13, 2001, 17:52:15 ; Search time 15.26 Seconds
(without alignments)
484.875 Million cell updates/sec Run on:

US-09-105-1171-2 1091 1 DTPLEETMYALRDIVASGKA.....SHDAGINIWAKATDSKTREN 216 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	QI	· 4	YDJG_ECOLI	YCCK_BACSU	TAS_ECOLI	YAKC_SCHPO	YM98_MYCTU	AR72_HUMAN	AR73_HUMAN	AR71_RAT	STCV_EMENI	A115_TOBAC	YOKF_BACSU	IOLS_BACSU	GS69_BACSU	NORA_ASPFL	NORA_ASPPA	ALKE_BABBO	AADA_YEAST	AAD4_YEAST	AADE_YEAST	YDBC_ECOLI	AAD_PHACH	YJ66_YEAST	S6PD_MALDO	XYL1_PICST	AAD3_YEAST	IN22_MAIZE	MORA_PSEPU	YBJI_ECOLI	DCOP_TRIRE	CD97_HUMAN		DCOP_TRIHA
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ALIGNMENTS

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OI V	YAJO_ECOLI STANDARD; PRT; 324 AA.
255	01-NOV-1997 (Rel. 35, Created) 15-DEC-1008 (Del 37 Taet segmence indate)
77.	(Rel. 37,
GN	
SO	Escherichia coli.
38	Bacteria; Froteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
×	NCBL_TaxID=562;
N C	[1]
א ק ה	SECUENCE FROM N.A.
% X	MEDLINE=97426617; PubMed=9278503;
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA D	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mann B., Chao, V.
R.T.	"The complete genome sequence of Escherichia coli K-12.";
ы:	Science 277:1453-1474(1997).
N M	SPOTENCE FROM N A
RA	Jugotano India m. R. Araulo R., Abaricio A., Chung E., Davis K., Roberts D., Allen E., Araulo R., Abaricio A., Chung E., Davis K.,
RA	Iyman R., Kalman S., Komp C., Kurdi
RA 1	R.W.;
٦ <i>د</i>	SUBJECTED (AAN-1997) to the EMBLYCENDOUGHTCHER CACADASSES.
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U	between the Swiss Institute of Bioinformatics and the EMBL outstation
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ဗ္ဗ	entities requires a license agreement (see http://www.isb-sib.cn/announce/
ع د	of send an email to licensed sp.cn).
2 6	EMBL: AE000148: AAC73522.1: ALT INIT.
DR	EMBL; U82664; AAB40175.1; ALT_INIT.
DR	EcoGene; EG13611; yajo.
ΚM	xidoreductase.
F	ACT_SITE 127 127 HYDROGEN-BOND DONOR (PROBABLE).
) N	SEQUENCE 324 AA; 364ZU MW; UBO9EU9FZBEDF9BI CKC04;
Qu	Query Match 20.6%; Score 225; DB 1; Length 324; Best Local Similarity 31.9%; Pred. No. 4.2e-11;
Ma	vative 39
Qγ	₩.
Db	132 NTPIEETLEALNDVVKAGKARYIGASSMHASQFAQALELQKQHGWAQFVSMQDHYNLIYR 191
è	60 WVFFPGDDDGFNILOSAANNGLGVIAFSPLAGGLLTDKYLDGTPFGSRASOGKSL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A 32 kb nucleotide sequence from the region of the lincomycin-resistance gene (22-25 degree) of the Bacillus subtilis chromosome and identification of the site of the lin-2 mutation."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
254 --IDMLEQWQPLCARYQCTIPTLALAWILKQ-----SDLISILSGATAPEQVRENVAAL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL-DGIPEGSRASQGKSLSEGMLNV 120
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                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN NATB-RAPJ INTERGENIC REGION (ORFC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheng J., Guffanti A.A., Krulwich T.A.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 127 HYDROGEN-BOND DONOR (PROBABLE).
310 AA; 34800 MW; C06BF4195D25C91C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                310 AA
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Hypothetical protein; Oxidoreductase.
ACT_SITE 127 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kumano M., Tamakoshi A., Yamane K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB000617; BAA22238.1; -.
                                                                                                                                                                                                              306 NINLSDADATLMREMAEALE 325
                                                                                                                                                                 N-NLEFSDAEL ----EAID 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: 299105; CAB12071.1; -. EMBL: U30873; AAB53024.1; -. HSSP: P80276; 1AH3. SubtiList; BG11140; ycck. InterPro; IPR001395; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-268 FROM N.A.
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Matches 58; Conservative
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Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H.,
Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K.,
Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Tagami H., Takemoto K., Wada C., Yamanoto Y., Yano M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
  240 YKES-DENDAQIAERLIGVSEELGATRAQVALAWLLSKPG-----IAAPIIGTSREEDL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL-DGIPEGSRASQGKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                   SEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROGEN-BOND DONOR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 326;
                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN ANSA-RND INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1FF5C5252708978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 193; DB 1;
31.0%; Pred. No. 1.6e-08;
tive 40; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000272; AAC74841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36328 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D90821; BAA15569.1; -. D90820; BAA15562.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EcoGene; EG13483; ydjG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                            174 DNSLDSLN 181
                                                                                                                                                                                                           293 DELLNAVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                              YDJG_ECOLI
P77256;
15-JUL-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Pr
Escherichia.
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SEQUENCE
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  111 KSLSEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 --YKNLELYTKIEKIATANNITPGQLSLAWLLAQ----GDDIL--PIPGTKRVKYLEENF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 LNVNNIDMYRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSL 177
                         1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGS-RASQGKSLSEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy L., Niblett D., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 126 HYDROGEN-BOND DONOR (PROBABLE)
340 AA; 37710 MW; A4A9686A70968F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88; Indels
                                                                                                                                                                                                                                                                                                                                             SPACIF7.12 OR SPAC21E11.01.
Schlzosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schlzosaccharomycetes; Schlzosaccharomycetales; Schlzosaccharomycetales (Schlzosaccharomycetales).
                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 37.7 KDA PROTEIN C1F7.12 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.3%; Score 178; DB 1;
26.8%; Pred. No. 2.7e-07;
Live 42; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                           340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323
                                                                                                       171 EOLDNSLDSLNNLEFSD---AELEAIDEI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001395; -.
Pfam; PF00248; aldo_ket_red; 1.
Hypothetical protein; Oxidoreductase.
ACT_SITE 126
EQUENCE 340 AA; 37710 MW: A4A96R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 DSLNNLEFSDAELEAIDEISHDAGI 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P14550; 2ALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                         YAKC_SCHPO
009923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
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Matches
                                                                                                                                                                                                      YAKC_SCHPO
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                                          268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=B/R / WU3G10;
MFDDLINE=B/R / WU3G10;
Timms A.R., Bridges B.A.;
"Reversion of the tyrosine ochre strain Escherichia coli WU3G10 under straton conditions depends on a new gene tas.";
Genetics 148:1627-1635(1998).
-: SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGI-PEGSRAS-----QG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROGEN-BOND DONOR (BY S. 111692D06CA07CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.5%; Scole 100.0, ___
Best Local Similarity 30.1%; Pred. No. 1.7e-07,
Matches 63; Conservative 42; Mismatches 6
                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                      346 AA.
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00248; aldo_ket_red; 1.
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38499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U29581; AAB40481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000367; AAC75873.1;
EMBL; Y14609; CAA74961.1; -.
HSSP; P14550; ZALR.
                                                           181 NNLEFSDAELEAIDEI 196
                                                                                                   294 -NIELTEDEVNFISDI 308
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                  TAS_ECOLI STANDARD, Q4693; 15-JUL-1998 (Rel. 36, C) 15-JUL-1998 (Rel. 36, Le 15-DEC-1998 (Rel. 37, Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG13093; tas.
InterPro; IPR001395; -.
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                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                         TAS PROTEIN.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214
                     240
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MEDLINE=98244807; PubMed=9576847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%;
27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y16675; CAA76347.1; -. EMBL; AL035413; CAB72321.1;
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AKR7A2 OR AFAR OR AKR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                    SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             603418; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REDUCTASE.
                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                        TISSUE=Liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 MPGMRDLLDSGDIGAAGVSNYS---LARWRKADAALGRPVVSNQVHFSLAH-----PDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GENLLQSAANNGLGVIAFSPLAQGLLTDKY-LDGIPEGSRASQGKSLSEGMLNVNNIDMV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                     Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Taylor K., Whitehead S., Barrell B.G., Squres S., Sqares R., Sulston J.E. Techpering the blology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 MYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEEPGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 RKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSLNNLEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 ATLRAIAVDVDAKPAQVALAWLISLPG------VVAIPGASSVEQLE-----FNVAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR72_HUMAN STANDARD; PRT; 330 AA.
043488; 075749;
15-JUL-1999 (Rel. 38, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AFLATOXIN B1 ALDEHYDE REDUCTASE 1 (EC 1.-.-.) (AFB1-AR 1)
(ALDOKETOREDUCTASE 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 HYDROGEN-BOND DONOR (BY S
34986 MW; FF071A48B745B8E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.8%; Score 161.5; DB 1;
32.8%; Pred. No. 5.4e-06;
live 29; Mismatches 71;
                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculist; Rv2298; -.
Hypothetical protein; Oxidoreductase.
ACT_SITE 117 117 HYDROGEN
SEQUENCE 323 AA; 34986 MW; FF071A.
            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence u
30-MAY-2000 (Rel. 39, Last annotation
HYPOTHETICAL 34.9 KDA PROTEIN RV2298.
                                                                                                                                                                                                                        MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 277163; CAB00973.1; -.
                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Conservative
                                                                                 RV2298 OR MTCY339,12C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAELEA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIELSA 290
                                                                                                                                                                                                          STRAIN-H37RV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CAN MERABOLIZE THE AFLATOXIN BI (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGENIC EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                                                                                                                                                                                                  Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.;
"Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin Bl-aldehyde reductase.";
Biochem. J. 332:21-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 TPVEETLHACQRLHQEGKFVELGLSNYASWEVAEICTLCKSNGWILPTVYQGMYNATTRQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Praml C., Savelyeva L., Perri P., Schwab M.; "Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-1p36.1 in a region frequently altered in human tumor cells."; Cancer Res. 58:5014-5018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 VE-----TELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDGKQPVGRFFGNSWAETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROGEN-BOND DONOR (PROBABLE).
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3BBFB7ED0CAF4D54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 159.5;
Pred. No. 8e-
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AKR7A3.
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                             133 RNRYWKEHHFEGIALVEKALQAAYGASAPSMTSATLRWMYHHSQLQGAHG----DAVILG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VE-----TELFPCLRHFGLRFYAFNPLAGGLLTGKYKYEDKNGKQPVGRFFGNTWAEMY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E -> D (IN REF. 1).
V -> M (IN REF. 1).
A -> AQQSPEGGGSFWGTLGPGADCCFPS (IN REF. 2).
N -> D (IN REF. 1).
B9C32C33C7102AB3 CRC64;
                                                                                                                                                                                     Knight L.P., Primiano T., Groopman J.D., Kensler T.W., Sutter T.R., "CDNA cloning, expression and activity of a second human aflatoxin B1-metabolizing member of the aldo-keto reductase superfamily,
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROGEN-BOND DONOR (PROBABLE)
                                                         01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AFLATOXIN B1 ALDEHYDE REDUCTASE 2 (EC 1. - . -) (AFB1-AR 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 157.5; DB 1;
; Pred. No. 1.2e-05;
30; Mismatches 98;
                             331 AA.
                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                            MEDLINE-99315412; PubMed-10383892;
                                                                                                                                                                                                                               Carcinogenesis 20:1215-1223(1999).
                           AR73_HUMAN STANDARD; F 095154; O9NUC3; 01-0CT-2000 (Rel. 40, Created) 01-0CT-2000 (Rel. 40, Last sequel 01-0CT-2000 (Rel. 40, Last sequel 01-0CT-2000 (Rel. 40, Last sequel of 01-0CT-2000 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF040639; AAD02195.1; -. EMBL; AL035413; CAB72322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00069; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37206 MW;
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27.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215
323
                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
323
331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00069
Oxidoreductase
                                                                                                                                                                  TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                           AKR7A3
        RESULT 8
AR73_HUMAN
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-1- FUNCTION: CAN METSABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
-1- FUNCTION: CAN METSABOLIZE THE AFLATOXIN B1 (AFB1) DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knight L.P., Primlano T., Groopman J.D., Kensler T.W., Sutter T.R.; "CDNA cloning, expression and activity of a second human aflatoxin B1-metabolizing member of the aldo-keto reductase superfamily,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93364879; PubMed=8395332; MEDLINE=93364879; PubMed=8395332; Hayes J.D., Judah D.J., Neal G.E., Resistance to aflatoxin B1 is associated with the expression of novel aldo-keto reductase which has catalytic activity towards a cytotoxic aldehyde-containing metabolite of the toxin."; Cancer Res. 53:3887-3894(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FISCHER 344; TISSUE-Liver;
MEDLINE-94052160; PubMed-8234296;
Ellis E.M., Judah D.J., Neal G.E., Hayes J.D.;
"An ethoxyquin-inducible aldehyde reductase from rat liver that metabolizes aflatoxin B1 defines a subfamily of aldo-keto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 156.5; DB 1; Length 327; Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AFLATOXIN B1 ALDEHYDE REDUCTASE (EC 1.-.-.) (AFB1-AR).
AKR7A1 OR AFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROGEN-BOND DONOR (PROBA 7427F3383AC190FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 6-17; 89-97; 156-184; 232-246 AND 250-274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reductases.";
Proc. Natl. Acad. Sci. U.S.A. 90:10350-10354(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raymackers J., Anderson L.;
Submitted (NOV-1994) to the SWISS-PROT data bank.
                                                                                                                                                                                                                              327 AA.
167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
                                      289 MSSLEQLEQNLAAAEEGPLEPAVVDAFNQAWH 320
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                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=99315412; PubMed=10383892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36742 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X74673; CAA52740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFFECTS OF AFLATOXIN B1
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase.
ACT_SITE 109
SEQUENCE 327 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                 AR71_RAT
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117 MLNVNNID-----MVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVE 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001395; -. Pfam; PF00248; aldo_ket_red; 1.
                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQKF_BACSU STANDARD; I P54569; 01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 H
33857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X56267; CAA39708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. WHITE BURLEY;
van der Zaal E.J.;
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31,
01-FEB-1995 (Rel. 31,
15-JUL-1998 (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S16390; S16390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 SSVEQLDNSL 177
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292 TKIENLNQNM 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136
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                                                                                                                                                                                                                                                     A115_TOBAC
P40691;
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01-FEB-1995
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SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
8
                                                                        61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                            118 L------NVNNIDMVRK-LNDIAQERGOSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                      229 MDRYWKEEHFNGIALVEKALKTTYGPTAPSMISAAVRWMYHHSOLKGTQG----DAVILG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSL---SEG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- QYKSAEEFQQEG 250
       Gaps
                                            TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCP-LLIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown D.W., Yu J.-H., Kelkar H.S., Fernandes M., Nesbitt T.C.,
Keller N.P., Adams T.H., Leonard T.J.;
"Twenty-five coregulated transcripts define a sterigmatocystin gene
cluster in Aspergillus nidulans."
Proc. Natl. Acad. Sci. U.S.A. 93:418-1422(1996).
-I- FUNCTION: MAY BE INVOLVED IN THE DEHYDRATION OF 5'-
HYDROXXAVERANTIN TO FORM AVERUFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emericella nidulans (Aspergillus nidulans).
Bukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; Emericella.
NCBI_TAXID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROGEN-BOND DONOR (POTENTIAL). : 1621588273B85E8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: STERIGMATOCYSTIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PUTATIVE STERIGMATOCYSTIN BIOSYNTHESIS DEHYDROGENASE STCV
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
94;
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                                                                                                                                                                                                                                                                                                                  167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
                                                                                                                                                                                                                                                                                                                                              285 MSSLEQLEQNLALVEGPLEPAVVDAFDQAWNLVAHE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 152.5; DB 27.0%; Pred. No. 3.6e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 AA
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACSYRDFEREILPMCQSEGLALAPWGALGRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=FGSC 26;
MEDLINE-96202293; PubMed=8643646;
  37;
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43548 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U34740; AAC49206.1;
    Conservative
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Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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ACT_SITE 148
SFOHENCE 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STCV_EMENI
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    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                         ---SPYVFPVIGCRTVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLN--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 RKYLPRFQAENLENNKNLYERICEMAVRKGCTPSQLALAWVHQ----GND--VCPIPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VINIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jan 21 Jan 2017.

21 INDUCTION: BY AUXIN

-! - SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROGEN-BOND DONOR (PROBABLE).
C4417DA852613360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 1; Length 307; 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59; Indels
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
AUXIN-INDUCED PROTEIN PCNT115.
                                                                                                                                                                                                                                                                                                       307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 150;
Pred. No. 4
                                                                                     172 OLDNSLDSLNNLEFSDAEL-EAIDEISHDAG 201
                                                                                                                     305 QLEANITSL-GVELSDEEIYEIEDTIPFDVG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDG--IPEGSRASQGKSLSEGMLN 119
                                                                                                                                                                                                                                                                                                                                                                          Hecker M.;
"First steps from a two-dimensional protein index towards a response-
                                                                           [2]
SEQUENCE FROM N.A.
STRAIN=168 / BGSC1A1;
Fujita Y., Shibayama T., Ishio I., Aoyama D., Yoshida K.-I.;
"Organization and transcription of the myo-inositol operon, iol, of Bacillus subtilis.";
  "Cloning and sequencing of a 36-kb region of the Bacillus subtilis genome between the gnt and iol operons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-----KIFFPYTKEHNISFIPYFPLVSGLLAGKYTEDTTFPEGDLRNEQEHF-KGERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 VNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 KENIRKVNKLAPIAEKHNVDIPHIVLAWYL-----ARPEIDILIPGAKRADQL----
                                                                                                                                                                                                                                                                                                                                                                                                                       regulation map for Bacillus subtilis.";
electrophoresis 18:1451-1463(1997).
-!- PATHWAY: MYO-INOSITO. CAPABOLISM.
-!- PATHWAY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                              Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROGEN-BOND DONOR (PROBABLE)
A870F226F8684867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 310;
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                                                                                                                                                                                                                         Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 9e-05; 37; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                         MEDLINE=97443988; PubMed=9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subtilist; BG11363; iols.
Pfam; PF00248; aldo_ket_red; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 H
35168 MW;
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HSSP; P23457; 1LWI.
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287 IDNIKTADVTLSQED 301
                                                  DNA Res. 2:61-69(1995).
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310 AA;
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Matches 49; Conserv
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                                                                                                                                                                                                                                                                         SEQUENCE OF 1-20.
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SEQUENCE
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GS69_BACSU
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                                                                                                                                                                                                                                                                    Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S., Sabto T., Takeuchi M., Sabor T., Takeuchi M.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 146; DB 1; Length 306; 25.5%; Pred. No. 8.9e-05;
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MEDLINE-96093926; PubMed=7584049;
Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;
                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 32, Last sequence update) 10LS PROTEIN (VEGETATIVE PROTEIN 147) (VEG147) 10LS OR SS92ER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D84432; BAA12638.1; -.
EMBL; Z99116; CAB14294.1; -.
Subtilist; BG11761; yqkF.
InterPro, IPR001395; -.
Pfam: PF00248; aldo_ket_red; 1.
Hypothetical protein; Oxidoreductase.
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01-NOV-1995 (Rel. 32, Last sequ
30-MAY-2000 (Rel. 39, Last anno
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Matches 50; Conservative
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282 RRLTEEEIKALQ--SH 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 PIEETAEVMKELYDAGKIRAIGVSNFSIE---OMDTFRAV--APLHTIQPPYNLFEREME 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 EPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL-----DGIPEGSRASQGKSLSE 115
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                                                                         -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, LIMITATION AND OXYGEN LIMITATION.
-1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                      Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., Submitted (JUN-1997) to the EMBL/GenBank/DDbJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROGEN-BOND DONOR (PROBABLE).
                                                                                                                                                                                                                                                                              Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
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82BC24D46E4994D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 SLD----SLNNLEFSDAELEAIDEISHDAGINIWAKAT 209
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NORSOLORINIC ACID REDUCTASE (EC 1.1.1.-).
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                                                                                                                                                                                                                                                                                                                                                      regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y14082; CAA74498.1; -.
EMBL; 299109; CAB12792.1; -.
HSSP; P23457; ILWI.
SubtiList; BG13020; yhdN.
Pfam; PF00248; aldo_ket_red; 1.
Oxidoreductase; Heat shock.
ACT_ETE 125 HYDR
CONFLICT 25 25 G->
                                                                                                                                                                                                                                            MEDLINE-97443988; PubMed-9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37312 MW;
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                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                            SEQUENCE OF 1-25.
  NCBI_TaxID-1423;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NRRL 3357;
MEDLINE=96156784; PubMed=8593042;
Cary J.W., Wright M., Bhatnagar D., Lee R., Chu F.;
"Molecular characterization of an Aspergillus parasiticus dehydrogenase gene, norA, located on the aflatoxin biosynthesis gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNIDMVRKINDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSL
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Pred. No. 0.00041;
9; Mismatches 84; Indels 23
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25.1%; Pred. No. 0.00°
tive 39; Mismatches
                                                                                                                                                                    62:360-366(1996).
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Best Local Similarity 25.1%
Matches 49; Conservative
                                                                                                                                                                  Environ. Microbiol.
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Search completed: September 13, 2001, 17:57:09 Job time: 294 sec

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 GenCore version
Copyright (c) 1993 - 2000
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- protein search, using sw model OM protein September 13, 2001, 17:34:55 ; Search time 25.14 Seconds
(without alignments)
654.483 Million cell updates/sec Run on:

US-09-105-1171-2 1091 1 DTPLEETMYALRDIVASGKA......SHDAGINIWAKATDSKTREN 216 Title: Perfect score: Sequence:

Scoring table:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	0	G65086	E85959	T35337	B86873	A75289	H72391	T44988	C84256	F82815	r41659	E85538	C64771	T44934	B83093	T07394	A53131	866502	45312	F83170	866503	I59393	55463	D85787	C82294	D84315	T52133 ·	F69978	C64937	E75296
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	Score	529.5	526.5	449	366	283.5	267	257	238	237.5	227.5	225	225	213	211	209	209	208	208	206.5	205	205	205	197.5	197	196	195	194.5	193	193
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S75995 H83328	E82644 D82644 B69755	F85935 C65066 F72310	F/2218 T12582 S62584	T03384 S68409 H83427	H72307 S61978 C86176
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331	329 362 310	346 346	338 340	326 404 323	333 342 453
17.5	17.1 16.8 16.7	16.5	16.4 16.3	16.2 16.0 15.6	15.3 15.1 15.0
191	186.5 183.5 182.5	181.5	178.5 178	177 174.5 170	167 165 163.5
30	333	36.5	38 38	4 4 4 0 1 2	4 4 4 5 4 5

ALIGNMENTS

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hypothetical protein b3001 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: L2-sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Feb-2000
C;Accession: G65086
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A;Tetle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Residues: 1-346 <BLAT>
A;Roseidues: 1-346 <BLAT>
A;Cross-references: GB:AE000382; GB:U00096; NID:92367182; PIDN:AAC76037.1; PID:917893
A;Cross-references: GB:AE000382; GB:U00096; NID:655
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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14
1 DTPLEETMYALRDIVASGRALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW 60 11:11:11 11 11 11 11 11 11

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117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176 ð q

177 LDSLNNLEFSDAELEAIDEISHDAGINIWAKATD 210 δy

::|||| || || || :|| :|| :|| 312 VQALNNLTFSTKELAQIDQHIADGELNLWQASSD 345 g

RESULT 2
E85959
Probable reductase 24354 [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E85959
C;Accession: E85959
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, INTILLE 40, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

D.J.; May K.; Apoda

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Best Local Similarity
Matches 68; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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A:Accession: E85959
A;Status: preliminary
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nesidues: 1-346 <STO>
A;Cross references: GB:AE005174; NID:g12517567; PIDN:AAG58137.1; GSPDB:GN00145; UWGP:Z43
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4354
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cydrocesion: T35337
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1999
A;Reference number: 221575
A;Reference number: 221575
A;Accession: T35337
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-319
A;Cross-references: EMBL:AL049863; PIDN:CAB42946.1; GSPDB:GN00070; SCOEDB:SC5H1.21c
A;Cross-references: EMBL:AL049863; PIDN:CAB42946.1; GSPDB:GN00070; SCOEDB:SC5H1.21c
A;Gene: SCOEDB:SC5H1.21c
C;Genetics:
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable ion channel subunit - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov_1999 #sequence_revision 05-Nov-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 MLTEANLNSLRLLNEMAQQRGQSMAQMALSWLLKD-----ERVTSVLVGASRAEQLEEN 311
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Superfamily: fission yeast pyridoxine 4-dehydrogenase
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48.3%; Score 526.5; DB 2;
Best Local Similarity 50.9%; Pred. No. 5.3e-34;
Matches 109; Conservative 39; Mismatches 51;
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41.2%; Score 449; DB 2;
Best Local Similarity 53.6%; Pred. No. 5.8e-28;
Matches 105; Conservative 25; Mismatches 54
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GNLDFDADELARIDKI 316
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A;Cross-references: GB:AE002063; GB:AE000513; NID:g6460121; PIDN:AAF11861.1; PID:g646
A;Experimental source: strain Rl
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                                                                                                                                                                                                    J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: DNA
A Molecule type:
A Molecule type:
C Molecu
oxidoreductase yugB [imported] - Lactococcus lactis subsp. lactis (strain IL14( C;Species: Lactococcus lactis subsp. lactis (c;Bate: 13-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001 (C;Batession: B86873 # R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. in press, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG--KSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEE-GCPLLIHQPSYSIINR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                         A;Title: The complete genome sequence of the lactic acid bacterium. A;Reference number: A86625 A;Accession: B86873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: DR2317
A;Map position: 1
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%; Score 283.5; DB 2;
llarity 34.5%; Pred. No. 5.7e-15;
Conservative 40; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.5%; Score 366; DB 2; 54.6%; Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 LNVNNIDMVRKLNDIAQERGQSLAQMALAWVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.59
Best Local Similarity 54.69
Matches 83; Conservative
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probable oxidoreductase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84256
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       voltage-gated potassium channel beta subunit XF0367 [imported] - Xylella fastidiosa C; Species: Xylella fastidiosa
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A;Cross-references: GB:AE004437; NID:g10580553; PIDN:AAG19415.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                    SYLTEENFDYHDELDAVAGEVDATPAQTALAWLMHRDG-----VTAPIVGARTVEQLTE 308
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                                                                                                                                                                                                                                                                                                                                                                         116 GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQGKSLSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDN 175
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                             1 DTPLEETMYALRDIVASGKALYVGISSYGPEL--TAEAAEFMAEEGC-PLLIHQPSYSII
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                                                                                                                                        18;
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                                                                                         Length 336;
                                                                                                                                        84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: yajO2
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
A;Note: expressed during exponential growth
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%; Score 238; DB 2;
33.5%; Pred. No. 2.3e-11;
tive 34; Mismatches 81;
                                                                                         ; Score 257; DB 2;
; Pred. No. 7.5e-13;
40; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 NLEAA-TIDLTDEQVDRLTGAKPDPYVGL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDSLNNLEFSDAELEAIDEISHDAGINI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 SLDSLNNLEFSDAELEAIDE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|: :: :| :: : : : NIDAA-TIDLTDDQMARLTD 327
                                                                                       ch 23.6%;
1 Similarity 32.1%;
67; Conservative 40
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: DNA
                                                                                         Query Match
Best Local S
Matches 67
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A;Molecule type: DNA
A;Residues: 1-319 <ARN>
A;Cross-references: GB.AE001713; GB:AE000512; NID:g4980809; PIDN:AAD35401.1; PID:g498081
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                              C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72391
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sed A;Reference number: A72200; MUID:99287316
A;Accession: H72391
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C;Species: Haloferax volcanii
C;Species: T4488
S;Farahani, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois, R.L. submitted to the EMBL Data Library, March 1997
A;Poscription: Hereditary instability of the megaplasmid pHV3, and filamentation in the A;Reference number: 222886
A;Accession: T44988
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                           SLSE-GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVEEPGDDGENLLQSAA----GK 111
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                     120 VNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%; Score 267; DB 2; Length 319; 33.8%; Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                K+ channel, beta subunit - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: TM0313
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
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A;Experimental source: strain DS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | :: | :: : | | :: | | :: | | :: | EQLEENLKAVEIKEKLTEDVMEEIEKILNE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQLDNSLDSLNNLE-FSDAELEAIDEISHD 199
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A; Genome: plasmid
                                                                                                                                            : || |::|
296 A-GVRLSDDVQRRIEDI 311
                                                                                                               180 LNNLEFSDAELEAIDEI 196
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A; Residues: 1-336 <FAR>
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25;

Indels

Length 344;

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A;Residues: 1-324 <STO>
A;Cross-references: GB:AE005174; NID:g12513275; PIDN:AAG54769.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable oxidoreductase (EC 1.....) yajo - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Feb-2000
C;Accession: C6477
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable NAD(P)H-dependent xylose reductase yajo [imported] - Escherichia ocisescies: Bscherichia coli c.bate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C.Accession: E85538 F.Perna, N.T. P. Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              258 PEGKTQLDQVRQISKIAEQIGATPSQLALAWTLKN-----PYVSTTILGASKPEQI--- 308
                                                                                                                                                                                                                        144 PMEEVVRAFTQLIQDGKAFYWGTSEWS-AFEIEHAHHIATKYNLIAPVADQPQYNYLTRD 202
                                                                                                                                                                                                                                                                                    61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                           121 ----nnidmvrklndiaqergqslaqmalawvlreqgeygadtvtsaligassveqldns 176
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                                                                                                                                                                3 PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL--LIHQPSYSIINRW
                                                                                                                                                                                                                                                                                                                         203 HFE-----KDLLPLQQIYGYGATVWSPLKSGILTGKYNDGIPEGSRLSTTFTSLAGQLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E85538 A;Status: preliminary
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                                                                                                 75;
                                        DB 2;
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                                                                     Pred. No. 1.6e-10;
                                                                                                 37; Mismatches
                                        Score 227.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 VENVKAVEFIDKLTPEILKKIDEI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 LDSLNNLEFSD----AELEAIDEI 196
                                     20.9%;
                                                                                                 67; Conservative
                                                                     Best Local Similarity
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                                        Query Match
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                                                                                                                                                                                                                                                                                                                         A.Cross references: GB.AE003888; GB.AE003849; NID:g9105187; PIDN:AAF83177.1; GSPDB:GN001
A.Experimental source: strain 9a5c
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.F. Facincani, A.P.; Ferreira, A.J.S.
A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramec, E.E.; Laigr A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.E.M.; Marques, M.V.; Martins, F.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Marques, M.V.; Martins, F.A.; Authors: da Silva, A.C.R.; da Silva, A.M.; Gasa, A.J., de M.A.; da Silva, A.M.; Silva Jr., W.A.; Gasilvai, T.Shako, M.H.; Vallada, H.; Van Sluys, M.A.; Valjovski-Almeida, S.; Vettore, A.L.; Z. A.Contents: annotation
                                                              R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
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Gispectes: Schizosaccharomyces pombe
Gispectes: Schizosaccharomyces pombe
Gispectes: 3-bec-1999 #sequence_revision 03-bec-1999 #text_change 18-Feb-2000
Giacesion: T41659
Riwood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
Rajandream, M.A.; Barrell, B.G.; Rieger, M.
A.Rocession: T41659
A.Rocession: T41659
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Rosiques: 1-344 <WOO>
A.Coss-references: EMBL:AL023590; PIDN:CAA19066.1; GSPDB:GN00068; SPDB:SPCC965.06
A.Experimental source: strain 972h-; cosmid c965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRA-----SQGKS 112
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                                                                                                                    A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A83515; MUID: 30365717
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <SIM>
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.Map position: 3
:Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: XF0367
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKENLRALQVVAALDA 376
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D.J.; May K.; Apoda

J.D.; Rose, Potamousis,

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Length 324;

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probable oxidoreductase PA4434 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Sacession: B83093
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L., Lory, S.; Olon, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A; Reference number: A82950; MUD:20437337
A; Accession: B83093
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-345 <STO>A; Cross-references: GB:AE004857; GB:AE004091; NID:g9950654; PIDN:AAG07822.1; GSPDB:GN
A; Experimental source: strain PAO1
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----GRKAVTSIII 288
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Best Local Similarity 33.0%; Pred. No. 3.2e-09;
Matches 66; Conservative 33; Mismatches 85; Indels
     240 WTEPPVRDEERLWNI-----VDTLLSVADGRGVSAAQVALAWLI---
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
C;Keywords: voltage-gated ion channel
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1.130 < CELG>
A,Cross-references: EMBL:AJ000999; PIDN:CAA04451.1
A,Experimental source: cv. Desiree
                                                                                                                                       319
                                                                                   197
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GGRTEAQFKDNL-AAADLQLSAEERKRLDDVS
                                                                                     GASSVEQLDNSLDSLNNLEFSDAELEAIDEIS
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321 V-DLRLDEEVLAGIDAIHRE 339
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                                                                                                                            A Molecule type: DNA

A Residues: 1-348 < BLAT>

A Cross-references: GB:AE000148; GB:U00096; NID:g1786614; PIDN:AAC73522.1; PID:g1786621;

A Experimental source: strain K-12, substrain M01655

C; Genetics:

A, Gene; yajo

C; Superfamily: fission yeast pyridoxine 4-dehydrogenase

C; Keywords: oxidoreductase

F;151/Active site: His #status predicted
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R;Kim, K.S.; Farrand, S.K.
Bacteriol. 178, 3275-3284, 1996
A;Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mar by the plant tumor.
A;Reference number: 222872; MUID:96236046
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C;Species: Agrobacterium tumefaciens
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-354 <KIM>A; Residues: 1-354 <KIM>A; Cross-references: EMBL: U19620; NID: 9797330; PIDN: AAB07785.1; PID: 9797336
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ-----GKSL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 SEGMLNVNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 YKES-DENDAQIAERLIGVSEELGATRAQVALAWLLSKPG-----IAAPIIGTSREEDL 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSIINRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPLEETMYALRDIVASGKALYVGISSY-----GPELTAEAAEFMAEEGCPLLIHQP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .197
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                                                                             Accession: C64771
Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 354;
cience 277, 1453-1462, 1997
Title: The complete genome sequence of Escherichia coli K-12.
Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity 32.5%; Pred. No. 2.3e-09;
Matches 69; Conservative 35; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.6%; Score 225; DB 2; Best Local Similarity 31.9%; Pred. No. 2.6e-10; Matches 60; Conservative 39; Mismatches 63.
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317 DELLNAVD 324
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A;Genome: pla
C;Superfamily
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Ouery Match
19.2%; Score 209; DB 2; Length 330;
Best Local Similarity 30.5%; Pred. No. 4.3e-09;
Matches 64; Conservative 40; Mismatches 70; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 RWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDG-IPEGSRASQGKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 LNVNNI------DMVRKLN----DIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGA 167
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Search completed: September 13, 2001, 17:52:41 Job time: 1066 sec 30, Appl 2, Appli 6, Appli 2, Appli 216, App 28, Appli 4, Appli 4, Appli 19, Appli 19, Appli

us-09-105-117i-2.rai (1m E

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COMPOUNDS AND RELATED METHODS FOR MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
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                 Sequence 4
Sequence 2
Sequence 4
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BATENIN Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/606,143

FILING DATE: 23-FEB-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kilyk Jr., John

REGISTRATION NUMBER: 30763

REFERENCE/DOCKET NUMBER: 30763

TELECOMMUNICATION INFORMATION:
US-08-975-762-50
US-08-906-743-4
US-08-906-743-2
US-07-812-180A-2
US-08-312-180A-2
US-08-312-180A-2
US-08-1178-477B-2
US-08-178-477B-2
US-08-995-4
US-08-405-496A-28
US-08-405-496A-28
US-08-496-995-4
US-08-459-448A-19
US-08-459-448A-19
US-08-459-554A-19
US-08-459-504B-19
US-08-459-504B-19
US-08-459-448A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: COMPOUNDS AND RELATED METI:
    TITLE OF INVENTION: COMPOUNDS;
    TITLE OF INVENTION: COMPOUNDS
    NUMBER OF SEQUENCES: 45
    CORRESPONDENCE ADDRESS:
    CORRESPONDENCE ADDRESS:
    STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEEX: 25-3533
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 amino acids
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 TOPOLOGY:
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CITY: C
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(without alignments)
229.017 Million cell updates/sec
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Sequence 0, Al
Sequence 14, 1
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Sequence 22
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Patent No. 5
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                 version 4.5
- 2000 Compugen Ltd.
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US-08-907-626A-31

US-08-907-674-1

US-09-31-959-1

US-09-391-959-1

US-09-391-959-1

US-09-391-959-3

US-09-391-959-3

US-09-166-412-4

US-09-166-412-4

US-09-166-412-4

US-09-106-412-4

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US-08-459-448A-21
US-08-459-595A-21
US-08-459-504B-21
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JS-08-976-255-14
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                                                                                                                              September 13, 2001, 17:33:34
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Maximum Match 100%
Listing first 45 summaries
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                                                                                          OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                   GenCore
Copyright (c) 1993
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1091
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length: 2000000000
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95.5
82.5
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Maximum DB :
                                                                                                                                                                                                                                         Sequence:
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                                                                                                                              Run on:
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240 VSEEGRKQQNKLKDLSPIAERLGCTLPQLAVAWCLRNEG-----VSSVLLGSSTPEQLI 293
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 202; DB 2;
Pred. No. 3.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                           Sequence 2, Application US/08606143
Patent No. 5856155
                                                     175 NSLDSLNNL-EFSDAELEAIDEI 196
                                                                                                     294 ENLGAIQVLPKMTSHVVNEIDNI 316
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TELECOMMUNICATION INFORMATION:
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31.2%;
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(312) 616-5700
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NAME: Kilyk Jr., John
REGISTRATION NUMBER: 3076
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Li, Min
TITLE OF INVENTION: COMI
TITLE OF INVENTION: COMI
TITLE OF INVENTION: COMI
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 64; Conserv
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STREET: TWC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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ZIP: 60601
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                                                                                                                                                                                                                  US-08-606-143-2
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125 NTPMEEIVRAMTHVINQGMAMYWGTSRWSAMEIMEAYSVARQFNMIPPVCEQAEYHLFQR 184
                                                  60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG--KSLSEGM 117
                                                                                 118 LNVNNIDMVRKLND---IAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLD 174
                                                                                                                                                                                         185 EKVE-----VQLPELYHKIGVGAMTWSPLACGIISGKYGNGVPESSRASLKCYQWLKERI 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOUNDS AND RELATED METHODS FOR
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUN
                                                                                                                                                                                                                                                                  175 NSLDSLNNL-EFSDAELEAIDEI 196
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TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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NAME: Kilyk Jr., John
REGISTRATION NUMBER: 3076
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1: 514
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 31.03
Matches 63; Conservative
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; MOLECULE TYPE: protein
US-08-606-143-3
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COMPOUNDS AND RELATED METHODS FOR .MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH COMPOUNDS 9 185 EKVE----VQLPELFHKIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKGYQWLKDKI 239 13 LSEGMLNVNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQ 172 1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEG-CPLLIHQPSYSIINR 59 22; Length 329; 60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRAS----Indels

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; Sequence 1, Application US/09215087; Patent No. 5981244
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                               TITLE OF INVENTION: HUNDBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY: BRAINOT14
; CLONE: 1596452
US-08-907-674-1
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   SENERAL INFORMATION:
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US-09-215-087-1
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          Sequence 31, Application US/08576626A

Patent No. 5998194

GENERAL INFORMATION:
APPLICANT: Summers, R.G.
APPLICANT: Katz, L.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.0%; Score 175; DB 2;
29.9%; Pred. No. 2.3e-10;
tive 38; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEX Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857.US.O1
TELECOMMUNICATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.08-907-674-1
Sequence 1, Application US/08907674
Patent No. 5919685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 31:
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LENGTH: 1114 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
Matches 59; Conserv
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US-08-576-626A-31
US-08-576-626A-31
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119 TPVEETLHACQRLHQEGKFVELGLSNYASWEVAEICTLCKSNGWILPTVYQGMYNAITRQ 178
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LN-----VNNIDMVRKLNDIAQ-ERGOSLAQMALAWVLRE---QGEYGADTVTSALIG 166
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: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 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APPLICANT: Shah, Purvi
PAPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: Fast5EO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,674
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bandman, Olga
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118 LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.9%; Score 162.5; DB 3; Length 331; 27.8%; Pred. No. 8e-10;
APPLICANT: COLIEY, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08907674
Patent No. 5919685
GENERAL INFORMATION:
APPLICANT: Brachan, Olga
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: COLley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                                                                                                                                                                          SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Mismatches
                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
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                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,959
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPHONE: 415-845-4166
                                                                                                             3174 Porter Drive
                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 331 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LIBRARY: BRAINOT14
; CLONE: 1596452
US-09-391-959-1
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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Matches 59; Conserv
                                                                                                                                     Palo Alto
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                               COUNTRY:
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US-08-907-674-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 RNRYWKEHHFEGIALVEKALQAAYGASAPSVTSAALRWMYHSQLQGAHG----DAVILG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 331;
                                                                   HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

14.9%; Score 162.5; DB

Best Local Similarity 27.8%; Pred. No. 8e-10;

Matches 59; Conservative 34; Mismatches 5
                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0362 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/215,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-391-959-1; Sequence 1, Application US/09391959; Patent No. 6071704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGA, OMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LIBRARY: BRAIN
; CLONE: 1596452
US-09-215-087-1
                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                            94304
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118 L-----DGEYGADTVTK-LNDIAQERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09391959

Patent No. 601704

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.3%; Score 156.5; DB 2
Best Local Similarity 26.3%; Pred. No. 3.6e-09;
Matches 57; Conservative 37; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 MSSLEQLEQULALVEEGPLEPAVVDAFDQAWNLVAHE 321
                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,087
FILING DATE:
    Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 327 amino acids TYPE: amino acid STRANDENNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank
                                         Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMEDIALL
LIBRARY: Generall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
                 3174
      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-391-959-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                         CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 L-----NVNNIDMVRK-LNDIAQERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 MDRYWKEEHFNGIALVEKALKTTYGPTAPSMISAAVRWMYHHSQLKGTQG----DAVILG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%; Score 156.5; DB 2; Length 327; 26.3%; Pred. No. 3.6e-09; Live 37; Mismatches 94; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09215087
Patent No. 5981244
GENERAL INFORMATION:
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                      ZIDENTIFY EADABLE FORM:
MEDION TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FASTSEN FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,674
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 MSSLEQLEQNLALVEEGPLEPAVVDAFDQAWNLVAHE 321
                                      SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0362 US
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/COCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 26.33
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LIBRARY: GenB;
; CLONE: 433611
US-08-907-674-3
                                                                                                                           USA
                                      ADDRESSEE:
                                                                                                     STATE: CA
                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-215-087-3
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TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNGANISM: apple IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 44; Conserv
                      Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: L. MOLECULE TYPE:
                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                         48864
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY:
US-09-166-412-4
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US-09-166-412-2
                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 MDRYWKEEHFNGIALVEKALKTTYGPTAPSMISAAVRWMYHHSQLKGTQG----DAVILG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.3%; Score 156.5; DB 3
Best Local Similarity 26.3%; Pred. No. 3.6e-09;
Matches 57; Conservative 37; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
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Patent No. 6133504
GENERAL INCRMATION:
APPLICANT: Wayne D. Loescher,
APPLICANT: Rebecca Grumet
TITLE OF INVENTION: DNA Encoding Mannose
TITLE OF INVENTION: A-Phosphate Reductase
TITLE OF INVENTION: and Recombinants
TITLE OF INVENTION: A-Phosphate Reductase
TITLE OF INVENTION: A-Phosphate Reductase
TITLE OF INVENTION: Produced Therefrom
                                                                                                                                        OPERATING SYSTEM: DOS
CUGFTURARE: FRSESED for Windows Version 2.0
CUGFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,959
                                                                                                                                                                                                                                                                                                                                                                           PF-0362 US
                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Is Ian C. McLeod
2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 433611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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Palo Alto
                                       USA
                                                                                                                                                                                                                  FILING DATE:
                                                       94304
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STREET: 21
                                       COUNTRY:
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64 PGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNVNNI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 107.5; DB 4; Length 310; 20.8%; Pred. No. 0.00091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 PYFORDSLVKFCMKHGVLPTAHTPLG-GAAANKDMFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wayne D. Loescher,
APPLICANT: John D. Everard
APPLICANT: Rebecce Grumet
TITLE OF INVENTION: DNA Encoding Mannose
TITLE OF INVENTION: 6-Phosphate Reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 QLSDEDMQLIYSIDRKYRTSLPSKTWGLDVYA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 EFSDAELEAIDEL -----SHDAGINIWA 206
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ian C. McLeod
REGISTATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-275
TELECOMMUNICATION INFORMATION:
                                                                                                   OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: (version 3.3)
SOFTWARE: Wordperfect 5.1
SOFTWARE: Wordperfect 5.1
APPLICATION NUMBER: US/09/166,412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 kb storage
                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/731,320
FILING DATE: October 15, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09166412
Patent No. 6133504
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APPLICANT: MIKIKO SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: OP813 CURRENT APPLICATION NUMBER: US/09/222,817 CURRENT FILING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: || || :| :| :| :| :| :| 10 DVPILETWKALEKLVKAGKIRSIGVSNFPGALLIDLLRGATIKPSVLQVEHHP----- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 YLQQP-----RLIEFAQSRGIAVTAYSSF------GPQSFVELNGGRALNTSPLF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 EN----ETIKAIAAKHGKSPAQVLLRW----SSQRGIAIIPKSNTVPRLLENKDVNSFD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLI-HQPSYSIINR 59
                                                                  APPLICANT: Penttila, Merja
APPLICANT: Ojamo, Heikki
APPLICANT: Keranen, Sirkka
APPLICANT: Han-Hagerdal, Barbei
APPLICANT: Waldfridsson, Mats
APPLICANT: Waldfridsson, Mats
APPLICANT: Waldfridsson, Mats
APPLICANT: Waldfridsson, Mats
APPLICANT: WITCH STEAM STEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.7%; Score 106; DB 2; Length 318; 24.2%; Pred. No. 0.0014; Live 36; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/336,198C
FILING DATE: 03-N0V-1994
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 N. Washington St. CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09222817; Patent No. 6037154; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
                                            Hallborn, Johan
Penttila, Merja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 318 amino acids
amino acid
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Best Local Similarity 24.2
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: 703-205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-198C-3
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COMPUTER READABLE FORM:
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288 -LDEQDFADIAKLD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-222-817-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 IDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSLNN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 DPVLKKLSD---KHNKSPAQIVLRW------GVQRNTIVIPKSSKTKRLEENI-NIFD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%; Score 106; DB 4; Length 309; 20.4%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Indels
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187 PYFQRDSLIKFCQKYGIAITAHTPLGGALANTERF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/731,320
FILING DATE: October 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lan C. WCLEGOD
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MGU 4.1-275
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 2:
                                        Produced Therefrom
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 kb storage
COMPUTER: 18M Compatible
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: (version 3.3)
SOSTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,412
TITLE OF INVENTION: and Recombinants TITLE OF INVENTION: Produced Therefr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 LEFSDAELEAIDEISHDAGINIWAKA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 FELSKEDMELIKTMERNQRSNTPAKA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08336198C Patent No. 5866382
                                                                                                   STATE: Michian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                     NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: celery IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                  STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ş
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MOLECULE TYPE:
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APPLICANT: MIXINO SUGA, MASARAZU SUGIMOTO, TSUYOSHI OSUMI, TSUYOSHI NAKAMATSU,
APPLICANT: MIXINO SUGA, MASARAZU SUGIMOTO, TSUYOSHI OSUMI, TSUYOSHI NAKAMATSU,
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OPRI3
CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT APPLICATION NUMBER: UP 10-3751
EARLIER FILING DATE: 1998-01-12
BARLIER FILING DATE: 1998-01-11
BARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING VET. 2.0
SEQ ID NO 14
LENGTH: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GLGVIAFSPLAQ--GLLTDKYLDGIPEGSRASQGKS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 ADSVLKALAGEFVADAVNVSGGRVGEEVAWMDLARKLGLLAGKLVDAAPVSIEVEARGE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 LSEGMLNVNNIDMVRKLND------IAQERG------OSLAQMALAWVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 REQGEYGADTVTSALIGASSVEQ------LDNSLDSLN-NLEFSDA--ELEAIDEISH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 VITGSGASATVVGALTGLERVEKITRINGRGLDLRAEGLNLFLQYTDAPGALGTVGTKLG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ALADAIESGHIRGAGFDVYSTEPCTDSPLFK----LPQVVVTPHLGASTEEAQDRAGTDV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 GENLLQSAANN------GLGVIAFSPLAQ--GLLTDKYLDGIPEGSRASQGKS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::|:: | ADSVLKALAGEFVADAVNVSGGRVGEKVAVWMDLARKLGLLAGKLVDAAPVSIEVEARGE 358
                                                                                                                                                                                                                                                                                                                                                                                                     10 ALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEEPG--DD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 95.5; DB 3; Length 530; 23.6%; Pred. No. 0.047; Live 30; Mismatches 106; Indels 5
                                                                                                                                                                                                                                                                                                          Length 530;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                        Query Match 8.8%; Score 95.5; DB 3; 1
Best Local Similarity 23.6%; Pred. No. 0.047;
Matches 59; Conservative 30; Mismatches 106;
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER PILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 12
LENGTH: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09222817 Patent No. 6037154
                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Brevibacterium flavum
US-09-222-817-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : TYPE: PRT
; ORGANISM: Brevibacterium flavum
US-09-222-817-14
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Best Local Similarity 23.6%
Matches 59; Conservative
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Db 359 LSSEQVDALGLSAVRGLFSGIIEESVTFVNAPRIAEERGLDISVKTNSESVTHRSVLQVK 418

Qy 150 REQGEYGADTVTSALIGASSVEQ------LDNSLDSLN-NLEFSDA--ELEAIDEISH 198

Db 419 VITGSGASATVVGALTGLERVEKITRINGRGLDLRAEGLNLFLQYTDAPGALGTVGTKLG 478

Qy 199 DAGINIWAKA 208

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Db 479 AAGINIEAAA 488

Search completed: September 13, 2001, 17:52:10

Job time: 1116 sec
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OM pi Run of Searc Searc Searc Searc Searc Datal Datal	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	protein - protein search, using sw model	on: September 13, 2001, 17:51:44; Search time 34.57 Seconds (without alignments) 508.561 Million cell updates/sec	<pre>nitle:</pre>	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 412676 segs, 60623988 residues	Total number of hits satisfying chosen parameters: 412676	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: A_Geneseq_0601:* 1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:* 2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 3: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:* 5: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 6: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 7: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 8: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 9: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 11: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 13: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 14: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 15: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 16: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 17: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 18: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 19: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 11: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 13: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 14: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 15: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 16: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 17: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 18: /SIDS8/gcgdata/geneseq/geneseqg/geneseqp/AA1991.DAT:* 20: /SIDS8/gcgdata/geneseq/geneseqgp/AA1991.DAT:* 21: /SIDS8/gcgdata/geneseqg/geneseqgp/AA1999.DAT:* 22: /SIDS8/gcgdata/geneseqg/geneseqgp/AA1999.DAT:* 23: /SIDS8/gcgdata/geneseqg/geneseqgp/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	C. glutamicum Lys	Corynebacterium ql	ORFL16 protein inv	SnpR activator pro	Amino acid sequenc	Neisseria meningit	Neisseria meningit	Protein encoded by	Amino acid sequenc	S. venezuelae macr	Narbonolide syntha
	ID	AAW37714	AAB79658	AAY39317	AAW36129	AAB30494	AAY74592	AAY74593	AAY29277	AAB18640	AAY77195	AAY67204
	DB	18	22	50	19	21	21	21	20	21	21	21
	Match Length DB	290	290	278	311	311	299	299	344	1346	1346	1346
* O	Match	100.0	100.0	8.1	7.2	7.2	7.0	7.0	6.9	6.8	6.8	6.8
	Score	1460	1460	118.5	105	105	102.5	101.5	100.5	99.5	99.2	99.5
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pik	gonorrhe	i ri	>	ntib	ıg di	18 8,	prot	bios1	bioS1	QI I	QI I	8	C #2	pik	rans	IS OR	ulos	protein	protein	synthase	ngit	X ORF2255	sedneuc	macr	pik	syntha	d by	ıs 8,	anti	uvat	i ri	ide	synthase
venezuelae pik	ria gond	mediterranei	Truncated irgB.	omyces a	KSq-ATq loading d	antibioticus	bios1	d pHS1 h	d pHS1 b	1274 Sec	DE19731274 Seq	i biotir	Cephalosporin	enezuelae pik	promoter trans	. clavuligerus OR	Sorangium cellulos	tory pro	p57 pro	ose synt		ORFX OR		venezuelae macr	venezuelae pik	arbonolide sy	Protein encoded	. antibioticus	Cephalosporin ant	Phosphoenolpyruvat	A. mediterranei ri		
S. ven	Neisse	A. med	Trunca	Strept	KSq-AT	S. ant	E. coli	Plasmid	Plasmi	DE1973	DE1973	E. col	Cephal	S. ven	Bud pr	S. cla	Sorang	Regulatory p	Bovine p5	Cellulose	Neisseria	Human ORFX	Amino acid	S. ven	S. ven	Narbon	Protei	S. ant	Cephal	Phosph	A. med	SpnB a	Tylactone
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7180	6	2846	AAR25588	7292	8844	2707	AAY33264	AAY33268	3270	AAW92938	AAW92936	AAW92934	AAR49827	AAY77203	2378	AAR77865	AAY58577	0094	8342	5002	AAY95652	2491	AAB18638	7193	AAY77201	AAY67202	6467	AAY92708	AAR10691	6949	2848	AAY39298	2601
AAY771	AAY745	AAW5284	AAR2	AAY7729	AAY 788	AAY927	AAY3	AAY3	AAY3327	AAW9	AAW9	AAW9	AAR4	AAY7	AAW0237	AAR7	AAY 5	AAY8009	AAR9834	AAR4	AAY9	AAB4249	AAB1	AAY7719	AAY7	AAY6	AAB6646	AAY9	AAR1	AAR9694	AAW5284	AAY3	AAW2
21	21	19	13	21	21	21	20	20	20	20	20	20	15	21	17	16	21	21	17	14	21	21	21	21	21	21	22	21	12	17	19	20	18
12199	303	\$069	298	928	928	4150	401	401	401	401	401	401	383	1346	290	432	3798	303	461	1319	391	3266	3739	3739	3739	3739	2188	3816	419	856	1688	2152	4472
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99.5	86	95.5	93.5	92.5	92.5	92.5	92	92	92	92	92	92	89.5	89.5	89	87.5	87.5	87	86.5	86.5	86	84.5	84.5	84.5	84.5	84.5	83.5	83.5	83	83	83	82.5	82.5
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ALIGNMENTS

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99DE-1031434.
99DE-1031435.
99DE-1031443.
99DE-1031453.
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99DE-1031465.
99DE-1031478.
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                            This sequence is the LysG protein product, a lysine export regulator. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as plarmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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Query Match

Best Local Similarity 100.0%; Pred. No. 3.2e-150;

Matches 290; Conservative 0; Mismatches 0; Indels 0;
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         Disclosure; Page 6; 16pp; German.
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99DE-1030476.
99US-0142101.
99DE-1031415.
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01-JUL-1999;
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PR 03-SEP-1999; 99DE-1042076.
PR 03-SEP-1999; 99DE-1042076.
PR 03-SEP-1999; 99DE-1042077.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042098.
PR 03-SEP-1999; 99DE-1042098.
PR 03-SEP-1999; 99DE-1042098.
PR 03-SEP-1999; 99DE-1042098.
PR 03-SEP-1999; 99DE-1042124.
PR 03-SEP-1999; 99DE-1042129.
PR 03-SEP-1999; 99DE-1042129.
PR 03-SEP-1999; 99DE-1042124.
PR 03-SEP-1999; 99DE-1042129.
PR 03-SEP-1042129.
PR 03-SEP-104206.
PR 03-SEP-104206.
PR 03-SEP-10420
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Streptomyces sp.
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                                                                                                                                                                                                                                                                                                                                                                                               Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode; insect; polyketide; polyketide synthase; PKS; extender module; initiator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; Redotyl carrier formin; BH; enoyl reductase domain; ER; beta-ketoreductase; insecticide; transcriptional control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New spinosyn biosynthetic genes from Saccharopolyspora spinósa, useful for production of insecticidal spinosyn compounds
                                                                                                                     EVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTL 120
                                                                                                                                RLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLD 180
                                                                                                                                                                        WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240
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                                       Length 290;
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                                     100.0%; Score 1460; DB 22;
100.0%; Pred. No. 3.2e-150;
ive 0; Mismatches 0;
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Waldron C;
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                                                         Conservative
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Treadway PJ, Turner JR,
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                                               Similarity
         AA;
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inscrolides which are useful for the control of arachnids, nematodes and insects. Blosynthesis of spinosyns occurs via stepwise condensation and diffication of carboxylic acid precursors generating a linear polyketide which is modified further. The DNA sequence contains a central region of approximately 55kb which has homology to the DNA encoding the polyketide synthases (FKS) of known macrolide producers. The spinosyn PKS DNA region consists of 5 ORPS with stop codons at the end of acyl carrier protein (ACP) domains. Together the PKS polypeptides (AAX39297-X39301), form a complex consisting of an initiator module, spnA, and several extender modules spnB-spnE. The products of the genes present in the region upstream of the PKS genes have been assigned names spnB-spnS region upstream of the PKS genes have been assigned names spnB-spnS spinosyn blosynthesis. There are also two ORFS ORFL15 and oRFL16 present immediately upstream of spnS, producing polypeptides AAX39318-Y39319. It is suggested that the ORFL16 producing polypeptides AAX39318-Y39319. It is suggested that the ORFL16 producing polypeptides AAX39318-Y39319. It is suggested that the ORFL16 protein is involved in transcriptional control during spinosyn and in spinosyn biosynthesis. The modified spinosyns may be a new insect on repinosyn biosynthesis. The modified spinosyns may be a new insect in spinosyn biosynthesis. The modified spinosyns may be a new insect control agent or serve as substrates for further chemical modification and the creation of new semi-synthesis or other species by but is a production of new semi-synthesis or other species by but is a production of new semi-synthesis or other species by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 avdlllcesqpqktlhdgradv-allhqpfdptaeldieilnteqqvailpts-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 RGLGWGLLPETQAAPMLKA-GEVILLDEIPIDTPMYWQRWRLESRSLARL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18..39
/note= "alpha-helix-beta-turn-alpha helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.1%; Score 118.5; DB 20; Length 24.5%; Pred. No. 0.00015; ative 47; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW36129 standard; Protein; 311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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11;

s sp. strain C5, SnpA; S. venezuelae; alpha-amylase; cancer; tumour growth; angiogenesis.

99US-0129084.

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Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader
              Amino acid sequence of SnpR encoded by plasmid pANT1201
                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 9A-B; 57pp; English.
                                                                                                                                                            12-APR-2000; 2000WO-US09747.
                                                                                                                                                                                                                  (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                              Desanti CL, Strohl WR;
                                                                                                                                                                                                                                                                      WPI; 2000-686970/67.
N-PSDB; AAC62024.
                                                                                Streptomyces sp
                                                                                                        WO200060945-A1.
                                          Streptomyces
                                                                                                                                                                                       13-APR-1999;
                                                     endostatin;
                                                                                                                                   19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | :| | :| | :| | 68 srarplvaelcslvseara--'aavadaslrvgstasralagw----lrrlrhwqeptlh 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 QAARKMVL----LQAETKAQLSGRLAEIPLTIAINAD-SLSTWFPPVFNEVASWGGATLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 LRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQP-AKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                         activator gene. The snpR activator gene is incorporated in novel plasmid paWT195 (see AAV01451) that also includes the snpR-activated snpA promoter and a modified doxA gene (see AAV0147) of Streptomyces sp. strain C5. The doxA gene codes for daunomycin C-14 hydroxylase (see AAW36128), an enzyme capable of converting daunomycin to the anticancer agent doxcrubicin. Host cells, especially Streptomyces host cells, transformed with paNT195 can be used in methods for the production of doxcrubicin from daunomycin or for the hydroxylation and oxidation of other
                                                                                                                                                                                                               Producing doxorubicin from daunomycin by daunomycin C14 hydroxylase - also hydroxylation and oxidation of other anthracycline(s) with the same enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 DWAAMPVLRFGPKDVLQDRDLDGRVDGPVGR------RRVSIVPSAEGFGEAIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GLGWGLL--PETQAAPMLKAGEVILLDE--IPIDTPMYWQRWRLESRSLARLTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 vlraegldsrilhgdyhsaaylvatgevvtvvqptspsraetavrrlhgdplgvrlllaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 99
                                                                                                                                                                                                                                                                                               This protein is the encoded product of the Streptomyces snpR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 105; DB 19; 121.2%; Pred. No. 0.0052; ative 50; Mismatches 129;
                                                                                                                                               Strohl WA;
                                                                                                                                                                                                                                                                      Disclosure; Fig 6; 59pp; English.
                                                                                                                   (OHIS ) UNIV OHIO STATE. RES
                                                                97WO-US08690
                                                                                          96US-0653650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 21.29
Matches 66; Conservative
                                                                                                                                              Dickens ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 VVDAAIEGLRP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 rtdtelegvyp 278
                                                                                                                                                                         WPI; 1998-018495/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AA;
                                                                                                                                                                                     N-PSDB; AAV01451
           W09744439-A2
                                                                22-MAY-1997;
                                                                                          24-MAY-1996;
                                                                                                                                              DeSanti CL,
                                      27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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The present sequence is encoded by a fragment of pANT1201. This plasmid was used as a source of snpk, snph promoter, and multiple cloning site. The specification describes a method for the production of soluble, recombinant human endostatin in Streptomyces. Leader sequences of streptomyces sp. strain C5 Snph and S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 LRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 mdvsana-11rmvadghldvafvheve-----gslr---vpeglrvrvlvqrep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                srarplvaelcslvseara---aavadaslrvgstasralagw----lrrlrhwqeptlh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GLGWGLL--PETQAAPMLKAGEVILLDE--IPIDTPMYWQRWRLESRSLARLTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 21;
Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%;
21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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AAB30494 standard; Protein; 311 AA.

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AAB30494

06-MAR-2001 (first entry)

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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                            61 EVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPV-----FNE- 109
                                                                                                           -----VASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRH 161
                                                                                                                          NPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAG
                                                                                  64 agyfrragrilgemaaaetemla-vheipggvl----svdsampmvlhllaplaakfner
                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis ORF 158 protein sequence SEQ ID NO:660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grandi G,
Rappuoli R,
                                                                                                                                                                                                                                                 AAY74593 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                          antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US09346
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99US-0121528
                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petersen J, Pizza M,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis
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N-PSDB; AAZ53355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP
                                                                                                                                                            162 LAIATP 167
                                                                                                                                                                                      165 rviasp 170
                                                                                                                                                                                                                                                                                                                                                                                                                           WO9957280-A2
                                                                                                                                                                                                                                                                                                 21-MAR-2000
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
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09-OCT-1998;
25-FEB-1999;
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                                                                                                                                                                                                                                                                          AAY74593;
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                                                                                                                                                                                                                                      AAY74593
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                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE53015 to AAE54536, AAE54577 to AAE54615, and AAY74253 to AAY5941 represent novel Neisseria meningitis and N. gonorrheae polynocleotides and polypeptides. AAE5457 to AAE5456 and AAE54616 to AAE5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scarselli M;
208 vlraegldsrilhgdyhsaaylvatgevvtvvqptspsraetavrrlhgdplgvrlllaa 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mora M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                   Neisseria meningitidis ORF 158 protein sequence SEQ ID NO:658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V,
Scalato E, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hickey E,
Ratti G,
                                                                                                           AAY74592 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grandi G,
Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 452; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                        98US-0094869.
98US-0098994.
98US-0103749.
98US-0103749.
98US-0103796.
                                                                                                                                                                                                                         antigenic; diagnosis; immunantibacterial; gene therapy
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                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petersen J, Pizza M,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galeotti C,
                                                                                                                                                                                                                                                             Neisseria meningitidis.
                                      | :||: |
268 rtdtelegvyp 278
                       280 VVDAAIEGLRP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-062150/05
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                                                                                                                                                                                                                                                                                                                                    30-APR-1999;
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09-OCT-1998;
25-FEB-1999;
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02-SEP-1998
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                                                                                                                                   AAY74592
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                                                                                             AAY74592
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
                                                                                                                                                                                                                                                                          AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                              Claim 2; Page 453; 1453pp; English.
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Gaps

39;

67; Indels

7.0%; Score 102.5; DB: 26.3%; Pred. No. 0.0092; ative 31; Mismatches 6

Conservative

Query Match Best Local Similarity Matches 49; Conserv

DB 21; Length 299;

Masignani V, Mora M; Scalato E, Scarselli M;

Hickey E, Ratti G,

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27-MAY-1999;
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06-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAB18640;
                                          Seguence
                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                                                 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding by polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.
         be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
presence of Neisseria bacteria, or to raise antibodies. They may also
                                                                                                                                                                  EVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPV-----FNE- 109
                                                                                                                                                                               -----VASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRH 161
                                                                                                                                                                                                                           119 yphirlslvssegyinlierkvdia----lragel-----dasglrarhlfdsrf 164
                                                                                                       Gaps
                                                                                                                           9
                                                                                                                                        present sequence represents a Pseudomonas aeruginosa polypeptide
                                                                                                                        2 NPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAG
                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                  DB 21; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mahajan-Miklos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virulence factors useful in developing disease treatments
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                      67;
                                                                                 7.0%; Score 101.5; DB 26.9%; Pred. No. 0.012; iive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodman HM,
                                                                                                                                                                                                                                                                                                                        AAY29277 standard; Protein; 344 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 9; 228pp; English
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Tsongalis
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                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cao H,
Tan M, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357851/30
                                                                                         Local Similarity
es 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by
                                                  299 AA;
                                                                                                                                                                                                                                                                      165 rviasp 170
                                                                                                                                                                                                                                                   162 LAIATP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9927129-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rahme LG,
                                                                                                                                                                                                                                                                                                                                            AAY29277;
                              may also
                                                   Sequence
                                                                                 Query Match
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                                                                                            Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                     65 QAARKMVLLQAETKAQLSGRLAEIPLTIAINADS-----LSTWFPPVFNEVASWGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                       TLTLRLEDEAHTLSLLRR--GDVLGAVTREANPVAGCEVVE------LGTMRHL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 vvahpqhplcmaslhsiaslanyrqislgsrsgqhsmll-----rpvs-dkvlfve 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEVLV 64
in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is not entirely correct.
                                                                                                                                                                                                                                                                                                                                                                              pymrsllnyg----q1ig----diafnlnkgprnlrvlldtaippsfcd----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 AIATPS----LRDAYMVDGKLDWAAMPV-LRFGPKDVLQDRDLDGRVDGPVGRRRVSIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDEI----PIDTPMY-WQRWRLES-R
                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of narbonolide synthase subunit 4 (PICAIV).
                                                                                                                                                       Length 344;
                                                                                                                                                                                                       Indels
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                                                                                                                                                         DB 20;
                                                                                                                                                    ; Score 100.5; DB 20;
; Pred. No. 0.019;
47; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB18640 standard; Protein; 1346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Betlach M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                         6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0100880.
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                                                                                                                                  Query Match
Best Local Similarity 22...
70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces venezuelae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashley G, Betlach MC,
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                                                                                         344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 SLARLTDA 279
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e .g.

Desosamine and macrolide biosynthetic gene clusters, useful for,

Zhao L;

Sherman DH, Liu H, Xue Y,

WPI; 2000-160679/14.

N-PSDB; AA287300

(MINU) UNIV MINNESOTA

99WO-US14398 98US-0105537

25-JUN-1999; 26-JUN-1998;

06-JAN-2000.

WO200000620-A2

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The present sequence represents a narbonolide synthase subunit 4

(PICAIV). The nucleotide sequence encoding it is used in the course of the invention. The specification describes a recombinant DNA compound expressing recombinant polyketide synthase genes in host cells for the production of narbonolide, narbonolide derivatives and polyketides that are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl cransferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant of a compound relative to the unhydroxylated compound. The recombinant of the narbonolide polyketide synthase. These would be valuable for creating novel ketolide analogs for pharmaceutical applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 -----FPPVFNEVASWGGAT-----LTLRLEDEAHTLSLLRRGDVLGAVT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| ::|:| | ||::|
688 kggmislalseeatrgrienlh---glsiaavngptatvvsgdptgigelagaceadgir 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM------PVLRFGPKDV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   898 fqhrsywispagp-geapahtasgreavaet---glawgpgaedldeegrrsavlamvmr 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-----EVLVQAAR----- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neomethymycin; narbomycin; polyhydroxyaikanoate monomer synthase;
blopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma,
chronic obstructive pulmonary disease; respiratory inflammation;
hypercholesterolaemia; crop protection agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 wyrnlrhrvgfapavetlatdegfthfievsahpvltmtlpdkvtglatlrred-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 ariipvdyashsahvetieneladvlaglspqtpqvpffstle----gtwitepaldggy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 99.5; DB 21;
20.9%; Pred. No. 0.18;
live 35; Mismatches 107;
                                                                                                                             Disclosure; Columns 13-14; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY77195 standard; Protein; 1346 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 KAGEVILLD --- EIPIDTPM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   954 qaasvlrcdspeevpvdrpl 973
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Matches 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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production of biologically active macrolides. The macrolide biosynthetic production of biologically active macrolides. The macrolide biosynthetic production of biologically active macrolides. The macrolide biosynthetic neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biologically active agents, such as chemotherapeutics, impunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. Sequences AAY7190-Y77197 represent macrolide biosynthetic enzymes from second of the process of the content macrolide biosynthetic enzymes from the content and plants are encoded by sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purified nucleic acid segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 -KMVLLQ-----AFTKAQLSGRLAEIPLTIAINADSLSTW-----
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20.9%; Pred. No. 0.18;
Live 35; Mismatches 107; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-----EVLVQAAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated and
                                                                                                                                                                                                                                                                                                                                                                                  synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Page 424-428; 438pp; English.
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195 LQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE-----TQAAPML 244

Length 1346;

DB 21;

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06-JAN-2000.
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    Query Match
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  953
                                                                                                                                                                                                                                                                                                                                                 Narbonolide polyketide synthase; PKS; narbonolide synthase subunit 4; PICAIV; antibiotic production; narbomycin; picromycin; ketolide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the Streptomyces venezuelae narbonolide synthase subunit 4,
898 fqhrsywispagp-geapahtasgreavaet---glawgpgaedldeegrrsavlamvmr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
                                                                                                                                                                                                                                                                                                            Narbonolide synthase subunit 4 (PICAIV) protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 14-15; 98pp; English.
                                                                                                                                                                                  AAY67204 standard; protein; 1346 AA.
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                                                                               954 qaasvlrcdspeevpvdrpl 973
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                                                                                                                                                                                                                                                                 23-MAR-2000 (first entry)
                                        245 KAGEVILLD---EIPIDTPM
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces venezuelae
                                                              <del>:</del>
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N-PSDB; AAZ56001.
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22-SEP-1998;
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                                                                                                                                                                                                                          AAY67204;
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                                                                                                                                                                        898 fqhrsywispagp-geapahtasgreavaet---glawgpgaedldeegrrsavlamvmr 953
                                                                                                                                       ---EVLVOAAR---- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase;
blopolymer; antiblotic; chemotherapeutic; immunosuppressant; asthma,
chronic obstructive pulmonary disease; respiratory inflammation;
hypercholesterolaemia; crop protection agent.
                                                                                                                                                                                                                                                                                          195 LQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE-----TQAAPML
                                                                                                                                                                                                                                                                                                                                                                                                          REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM------PVLRFGPKDV
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                                                                                                                                                                                                                                                      -----AETKAQLSGRLAEIPLTIAINADSLSTW-
                                                                           107;
                                                                                                                                       19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-
6.8%; Scor.
20.9%; Pred. No. v...
... 35; Mismatches 10
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                                                                              Conservative
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                                                Best Local Similarity
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Scarselli Mora M;

Masignani V, Scalato E, S

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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAX75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54574 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Neisserial polypeptides predicted to be useful antigens for
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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Rappuoli R,
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                                                                                                                                                98US-0098994.
98US-0099062.
98US-0103749.
                                                         99WO-US09346
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98US-0103796
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Best Local Similarity 27.6%
watches 43, Conservative
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Tettelin H, Venter JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-062150/05.
                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ53353.
                                                                                                                                                                                               09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
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                                                         30-APR-1999;
            11-NOV-1999.
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02-SEP-1998
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biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, plikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be moromers. The compounds produced by the recombinant host cells are useful so biomomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat astima, chronic obstructive pulmonary disease as well as other diseases involving
                                                                                                                                                                                                                                                                                                                                    respiratory inflammation, cholesterol-Lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as protection agents (e.g., fungicides or insecticides) via expression of probyketides in plants: The present sequence represents a protein encoded by the macrolide biosynthetic gene cluster (pik) from streptomyces venezuelae ATCC 15439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM------PVLRFGPKDV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-----EVLVQAAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 -----FPPVFNEVASWGGAT-----LTLRLEDEAHTLSLLRRGDVLGAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 LQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE-----TQAAPML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 99.5; DB 21; Length 12199; 20.9%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AETKAQLSGRLAEIPLTIAINADSLSTW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrheae ORF 158 protein sequence SEQ ID NO:656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 4.6; 35; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY74591 standard; Protein; 303 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11526 qaasvlrcdspeevpvdrpl 11545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 KAGEVILLD---EIPIDTPM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 20.99
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 - KMVLLQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY74591;
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Gaps

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AAY74591

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The functional irgB gene encodes a protein which acts as a positive regulator of irgA. IrgA functions as a V cholerae virulence factor. The sequence given shows a truncated irgB. This truncation of the sequence inhibts expression of a functional irgA gene product in the cell. This sequence can be used to transform V. cholerae calls which can then be used to induce immunity to cholera in a mammal. These transformed cells can colonize the intestines of inoculated animals and may be combined with vaccines targeted at other illnesses to make a single multi-valent vaccine. The transformed cells have reduced virulence such that the inoculated animal is less likely to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cholera vaccine comprising live attenuated Vibrio cholerae cells - contains mutations which inhibit expression of a functional irgA gene product, vaccine has reduced virulence, decreasing side
                                                                                                                                                                                    Virulence factor; intestine; multi-valent vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            side effects such as diahhorea and fever
AAR25588 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 13; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calderwood SB, Goldberg MB,
                                                                                                                                                                                                                                                                                                                                                                      91WO-US09592.
                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0629102
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-250077/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ26543.
                                                                                                                                                                                                                               Vibrio cholerae.
                                                                                                                                      Truncated irgB.
                                                                                      08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1990;
                                                                                                                                                                                                                                                                             WO9211354-A.
                                                                                                                                                                                                                                                                                                                        09-JUL-1992.
                                             AAR25588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a Amycolatopsis mediterranel rifamycin synthesis gene cluster ORF B protein from the present invention. The DNA fragment comprises a DNA region involved directly or indirectly in the gene cluster responsible for rifamycin synthesis, including the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin biosynthesis, qualify as constituents of this rifamycin gene cluster, and functional fragments, derivatives or constituents of these. The Amycolatopsis mediterranel rifamycin synthesis gene cluster DNA fragment can be used for producing rifamycin, rifamycin analogues or precursors. It can also be used for inactivating or modifying genes involved in ansamycin or rifamycin biosynthesis. The DNA can be used for constructing mutant rifamycin biosynthesis gene cluster has been partly or completely deleted. The DNA fragment can be used for assembling a library of polyketide. The DNA fragment can be used for assembling a library of polyketides. A hybridisation probe of the invention can be used for identifying DNA fragments involved in the biosynthesis of ansamycins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4088 agivdggy-wy-----gfgpavaelvr 4115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4028 vvdalsgqevrvrrvavdygshtnqveaiedllaetlagieaqapkvpfystligdwird 4087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETKA-QLSGR--LAEIPLTIAINADSLSTWFPP-----VFNEVASWGGATLTLRLED 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAHTLS----LLRRGDV-LGAVTRE-----ANPVAGCEVVELGTMRHLAIATPSLRD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 AYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGL- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ASLALSISPSAVSQRV----KALEHHVGRVLVSRTQPAKATEAGEVLVQAARKMVLLQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                         Amycolatopsis mediterranei rifamycin synthesis gene cluster - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5%; Score 95.5; DB 19; Length 5
23.7%; Pred. No. 3.4;
Live 45; Mismatches 104; Indels
polyketide synthase; actinomycete; ansamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to produce rifamycin and rifamycin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 126-151; 205pp; English.
                                                                                                                                                                                    97WO-EP04495
                                                                                                                                                                                                                             96EP-0810551
                                             Amycolatopsis mediterranei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.7%
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                        Schupp T,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-169172/15.
N-PSDB; AAV21187.
                                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS AG
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                                                                                      WO9807868-A1
                                                                                                                                                                               18-AUG-1997;
                                                                                                                                                                                                                          20-AUG-1996;
                                                                                                                                    26-FEB-1998
                                                                                                                                                                                                                                                                                                                        Engel N,
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Mekalanos JJ;

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11;
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                                                                                                                                                                                                                                              EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSL---RDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                    ----kpt---hprelihhpwidf----iacrraelelhhpefgsyslpalesrlqsdnl 223
                                                                                                                                                                            18 sltaaakaleqpkstlsrrlaqleedlgqsllmrqgnrltltkagevfavyseqllelan 77
                                                                                                                                        17 SFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEV-----LVQAAR 68
                                                                                               71;
                                                                                                                                                                                                                                                                                                                                              132 sdevfepdli-----iwiehaapmgyrkerlgywryatyaspkylahrd----
                                                         Length 298;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                      180 DWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFG---
                                                     Score 93.5; DB 13;
Pred. No. 0.087;
                                                                                               Mismatches
                                                                                               33;
                                                     6.48;
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224 amgadaiakgrgigllp 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----EAIRRGLGWGLLP 236
                                                                                               Conservative
                                                       Query Match
Best Local Similarity
Matches 59; Conserv
298 AA;
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RESULT 15 P AAR25588

231 -GWGLLPETQAAPMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288

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Search completed: September 13, 2001, 17:51:47 Job time: 1118 sec



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307.477 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                             197339 seqs, 20590346 residues
                                                                                                                                               September 13, 2001, 17:52:10
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 27, App. Sequence 28, Sequence 4, Description Sequence 2 Sequence 1 Sequence 2 Sequence Sequence Sequence Sequence Sequence Sequence Sequence S Sequence Sequence Sequence Sequence Seguence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-320-878-4 L US-09-320-878-8 L US-09-320-878-8 L US-09-45-817-2 US-08-467-822-25 US-09-335-409-6 US-07-689-008-2 US-07-952-817-26 US-08-317-210A-2 US-09-113-825-2 US-08-185-432-17 US-09-320-878-2 US-08-469-005A-10 US-08-804-227C-14 US-09-413-814-105 US-08-463-092B-7 US-08-460-907B-7 US-09-413-814-76 US-09-036-987A-3 US-08-804-227C-2 SUMMARIES Query Match Length 829 1548 1548 591 3816 2152 Score 136.5 118.5 99.5 96 84. Result è

Appl Appl Appli Appli Appl Appli Appli Appl Appli

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Sequence 8, Appli Sequence 2, Appli		7	υ,	Sequence 2, Appli	Seguence 5, Appli	Sequence 11, Appl	Sequence 23, Appl	Patent No. 5210025	Sequence 2, Appli	Sequence 2, Appli	Sequence 89, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 2, Appli
US-08-804-227C-8 US-08-804-198-2	US-08-901-083-2 US-08-481-435-6	US-08-380-403A-2	US-08-380-403A-5	US-08-895-628-2	US-08-895-628-5	US-07-952-817-11	US-07-952-817-23	5210025-4	US-08-843-521-2	US-09-012-871-2	US-09-413-814-89	US-08-476-519-11	PCT-US95-09323-11	US-08-476-519-2	PCT-US95-09323-2
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4550	682	693	693	693	693	293	293	293	783	783	590	746	746	777	777
6.6.	5.0	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.4	5.4	5.4	5.4	5.4	5.4	5.4
81.5	81	81	81	81	81	80.5	80.5	80.5	79.5	79.5	79	78.5	78.5	78.5	78.5
5 5 7 7 8 8 8	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Keller, John W.

TITLE OF INVENTION: A Repressor Protein and Gene for Regulating
TITLE OF INVENTION: Expression of Polypeptides and Its Use in the Preparation o
TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%; Score 136.5; DB 1; Length 276; 23.9%; Pred. No. 3.1e-07; Live 29; Mismatches 110; Indels 81
                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,817
FILING DATE: 19920928
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 01120.0002-01000
                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                Sequence 27, Application US/07952817
Patent No. 5356796
GENERAL INFORMATION:
APPLICANT: Reller, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 202-408-4000 TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 276 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.9%
Matches 69; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-07-952-817-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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US-07-952-817-27
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COUNTRY:
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118 LTLRLEDEAHTLSLLR--RGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMV 175
                                                                                                                                     120 AVDLLLCESQPQKTLHDGRADV-ALLHQPFDFTAELDIEILNTEQQVAILPTS----- 171
  60 GEVLVQAARKMY--LLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGAT 117
                                                                                                                                                                                             176 DGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEG------FGEAIR 227
                                                                                                                                                                                                                                             172 ---HPLASEPHVRMADVSSLPDLPL-ARWPGPDG-----VYPDGPGVEVRNOTOLFOMIA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| ::|::| | | ||::|
688 KGGMISLALSEEATRQRIENLH---GLSIAAVNGPTATVVSGDPTQIQELAQACEADGIR 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------FPPVFNEVASWGGAT------LTLRLEDEAHTLSLLRRGDVLGAVT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM------PVLRFGPKDV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 WYRNLRHRVGFAPAVETLATDEGFTHFIEVSAHPVLTMTLPDKVTGLATLRRED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 -KMVLLQ------AETKAQLSGRLAEIPLTIAINADSLSTW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1346;
                                                                                                                                                                                                                                                                                            228 RGLGWGLLPETQAAPMLKA-GEVILLDEIPIDTPMYWQRWRLESRSLARL 276
                                                                                                                                                                                                                                                                                                                           223 IGRTTVVMPESSRVNLLEGLAAVPVLDAPDVTTVIAWPP-HSRSRALAGL 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION UNBER: US/09/320,878A
CURRENT PAPLICATION UNBER: US/09/320,878A
CURRENT PILING DATE: 1999-05-27
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-06-66
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
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EARLIER FILING DATE: 1998-02-08
EARLIER FILING DATE: 1998-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ASHLEY, Gary APPLICANT: BETLACH, Melanie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 300622002120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MCDANIEL, Robert APPLICANT: TANG, L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver.
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  --GG 115
                                                                                                                                     126 VTFDPQPALQGGELDLVMTSDILPRSELHYSPMFDFEVRLVLAPDHPLASKTQITPEDLA 185
                                          67 QLANQ-VLPQISRALQACNEPQQTRLRIAIECHSCIQWLTPALENFRASWPQVEMDFTSG 125
                                                                                                                                                                                             -----YELGTMRHL---AIATPSLRDA-----YMVDGKLDWAAMPVLRFGPK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Maddurl, Krishnamurthy
APPLICANT: Maddurl, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METRELRYFVAVAEELHFGRAAQRIGIAQPPLSRTIAQLEQRIGVVLLQRTSRKVSLTEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                        186 SETLLIYPVORSRLDVWRHFLQPAGISPLLKSVDNTLLLIQMVAARMGIAALPHW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 278;
                                                                                                                                                                                                                                                                                       193 DVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAA 241
                                                                                                                                                                                                                                                                                                                      65 QAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVF-NEVASW--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Fatentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%; Score 118.5; DB 4;
24.5%; Pred. No. 3.2e-05;
tive 47; Mismatches 139;
                                                                                             116 ATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV---
                                                                                                                                                                                                                                                                                                                                                                                                                             S-09-036-987A-22
Sequence 22, Application US/09036987A
Patent No. 6143526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 930 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 5
TELECOMMUNICATION INFORMATION
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 278 amino acids amino acid
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Best Local Similarity 24.5%
Matches 71; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-036-987A-22
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590 ALDEVCAELDTHLGRLL------GPEAGPPLRD-----VMFAERGTAHSALLSETHY 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  636 TQA----ALFALETALFRLLVQWGLKPDHLAGHSVGEIAAAHAAGILDLSDAAELVATRG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 SLLRR----GDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 LRFGPKDVLQDRDLDGRVDGPVGRR----RVS-----IVPSAEGFGEAIRRGLGWGLL 235
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                                                                                                                                                                                                            GENERAL INCOMMENTATION;
SURPLICANT: Betlach, Mary C.
APPLICANT: Betlach, Mary C.
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029,00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT APPLICATION NUMBER: 00/120,284
EARLIER FILING DATE: 1999-10-28
EARLIER PILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
SOFTWARE: PATENTIN VUMBER: 00/106,100
SOFTWARE: PATENTIN VOR: 2.1
SEQ ID NO 2
LENGTH: 4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AIEQILRDR-----GRKSRYLRVSHAFHSPLMEPVLEEFAEAVA----GLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.3%; Score 92.5; DB 4; Length 41 Best Local Similarity 23.3%; Pred. No. 1.7; Matches 70; Conservative 42; Mismatches 104; Indels
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APPLICANT: B CK, August; MAYER, Dagmar; SCHLENSOG, TITLE OF INVENTION: Express System Which Can Be NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Collard & Roe, P.C.
STREET: 1077 No. 5830692thern Boulevard
Sequence 1, Application US/08614686A Patent No. 5830692
                                                                                                                                                Sequence 2, Application US/09428517
Patent No. 6251636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-614-686A-1
                                                                                                                     US-09-428-517-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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TITLE OF INVENTION: A Repressor Protein and Gene for Regulating
TITLE OF INVENTION: Expression of Polypeptides and Its Use in the Preparation of
TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia
NUMBER OF SEQUENCES: 30
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Funnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                       69 KMVLLQAETKAQLSGRLAEIPLTIAIN - - ADSLSTWFPPVFNEVASWGGATLTLRLEDEA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 IVLHKEQLKLAIHKHHHLNQFAATGV----HLSQIIDEPMLLYPVSQKPNFATFIQSLFT 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 VTVVEEQSISKAAEKLCIAQPPLSRQIQKLEEELGIQLFERGFRPAKVTEAGMFFYQHA- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLVQAAR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 96; DB 1; Length 251;
21.7%; Pred. No. 0.0093;
Live 44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01120.0002-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/07/952,817
                                                                                                                                                                                                                                                                   Sequence 28, Application US/07952817
Patent No. 5356796
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/955
FILING DATE: 19920928
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0112
TELECHONE: 202-408-4000
TELECHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,146
                                                                                                                     954 QAASVLRCDSPEEVPVDRPL 973
                                                                                      245 KAGEVILLD --- EIPIDTPM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 251 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 21.7 tes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-07-952-817-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20005-3315
                                                                                                                                                                                                                                              US-07-952-817-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Labigne, Agnes
APPLICANT: Sauchbaum, Sebastien
APPLICANT: Sauchbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: INMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SA
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 QVLPAVPHLENAVQVEATEP----DGTKLVTVHDPISRENGELQEALFGSLLPVP---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 INADSLSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ----SLDK-----FAETKEDNRIPGEILCEDECLTLNIGRKAVILKVTSKGDRP----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 QRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 VELGTMRHLAIATPSL----RDAYMVDGKLDWAAMPVLRFGPKDVLQDR--DLDGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match .6.1%; Score 89; DB 2; Length 840; Best Local Similarity 22.1%; Pred. No. 0.36; Matches 59; Conservative 30; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995
                                                                      Sequence 25, Application US/08467822 Patent No. 5843460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    : 1300 I Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-467-822-25
                                                                                                                                                                                                                                                                                                                                                                                                                  Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 RKMVLLQA---ETKA---QLSGRLAE-IPLTIAINADSLSTW-----FPPVFNEVASWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GATLT------LRL---EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 IVPSAEGFGEAIRRGLGWGLLPETQAA------PMLKAGEVILLDEIPIDTPMYWQR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VAVAEARNFTRAAHDLGISQPPLSQQIQRLEREIGTPLLRRLTRGVELTEAGESFYVDAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGE-VLVQAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 RHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDV--LQDRDLDG--RVDGPVGR-RRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.1%; Score 89; DB 2; Length 290; Best Local Similarity 23.6%; Pred. No. 0.071; Matches 74; Conservative 56; Mismatches 105; Indels
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GR19510930
FILING DATE: 24 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Collard, Allison C.
REGISTRATION NUMBER: 22,532
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
ATTORNEY/AGENT INFORMATION:
NAME: FERENCE/DOCKET NUMBER: BOCK ET AL.-4
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: 26,048
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 365-9802
TELEFACO.: (516) 365-9805
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                        MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect Version 5.1
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/614,686A
FILING DATE: MARCH 12, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            омомитSM: Klebsiella terrigena
STRAIN: DSM2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Keusey, Edwin H. REGISTRATION NUMBER: 34,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 290 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 WRLESRSLARLTD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FE-RSRTVKRFLE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
New York
: U.S.A.
                                                                                                                                                                                                                                    FILING DATE: M
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                                        11576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-614-686A-1
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OY 204VDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE	PRESULT 9 195-085-029-10 196-085-029-10 196-09-185-029-10 196-185-029-11 196-185-029-029-029-029-029-029-039-039-039-039-039-039-039-039-039-03	Query Match 6.0%; Score 87.5; DB 4; Length 433; Best Local Similarity 33.7%; Pred. No. 0.19; Matches 29; Conservative 16; Mismatches 38; Indels 3; Gaps Oy 6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65 ::
OY 204VDGPVGRRRVSIVPSAEGFGBAIRRGLGWGLLPE	RESULT 8 15-08-08-431-697-25 15-08-08-431-097-25 15-08-08-097-25 15-08-08-097-25 15-08-097-25	Query Match Best Local Similarity 22.1%; Pred. No. 0.36; Matches 59; Conservative 30; Mismatches 114; Indels 64; Gaps 10; Qy 34 QRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIA 93 : :

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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-07-952-817-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 DPIEIEALRAVVGPARADGARCVL----GAVKTNLGHLEGAAGVAGLIKATLSLHHERIP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 RNLNFRTLNPRIRIEGTALALATEPVPWPRTGRTRFAGVSSFGMSGTNAHVVLEEAP--- 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 VLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDEAHTLS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVDGKLDWAAMPVLRF-----GPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 AVRGRASGGSAPKVVFVFPGQGSQWVGMGRKL--MAEEPVFR-----AALEGCDRAIEA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 EAGWSLIGELSADEAASQLGRIDVVQPVLFAMEVAL-----SALWRSWGVEPEAVVG 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AQAARLRDHLEKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 LLRRGDVLG--AVTREANPVAGCEVVELGTMRH-LAIATPS---LRDAY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGWGLLPETQA------APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Benžiman, Moshe
TITLE OF INVENTION: METHODS AND NUCLEIC ACID SEQUENCES FOR THE
TITLE OF INVENTION: EXPRESSION OF CELLULOSE SYNTHASE OPERON
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3798;
                                                                                                                APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Pevon
APPLICANT: Gorlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 87.5;
ilarity 22.2%; Pred. No. 5.3
Conservative 29; Mismatches
                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AVEPEAAAPERAAELFVLSAKSAAALD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VGRVLVSRTQPA----
                     Sequence 6, Application US/09335409
Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/07689008
Patent No. 5268274
                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Sorangium cellulosum
US-09-335-409-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ben-Bassat, Arie
Calhoon, Roger D
Fear, Anna L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gelfand, David H
Meade, James H
                                                                              APPLICANT: Schupp, Thomas APPLICANT: Ligon, James
                                                                                                                                                                                                                           FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tal, Rony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 HSMGEVAAA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 LTDAVVDAA 284
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6
LENGTH: 3798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
US-09-335-409-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-07-689-008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
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2120 LLAGLSPADYSPAIRSIAEEMEIKODLASRLSMVSNPVPLIREALTQPDPTGARGVAVAD 2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2288 PEÄ-----TSPKLALA--RLYNGHGKPGKALEIDLAVLRHNPQDLDARQAAVQAAVN 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2338 SDHNSLATRLAMDGVQESPMDARAWLAMAVADQADGHGQRTIEDLRRAYDLRLQQVEGTR 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 AAR-----KMYLLQAETKAQLSGRLAEIPLTIAINAD---SLSTWFPPVFNEVAS-- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 -----MGGATLTLRLEDEAHTLSLLRRG-----DVLG-----AVTREAN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 PVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKD------VL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2228 LLAPLGDGTGSATGSALLPEQVQTLQQLRMGISVAQSDLLNQRGDQAQAYDHLAPALQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/07952817
Patent No. 5356796
GENERAL INFORMATION:
APPLICANT: Keller, John W.
TITLE OF INVENTION: A Repressor Protein and Gene for Regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.5; DB
Pred. No. 4.9;
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 QDRD-----LDGRVDGPVGRR---RVSIVPSAEGFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LALSISPSAVSQRVKAL -- EHHVGRVLVSR-----
                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/689,008
FILING DATE: 19910422

CLASSIFICATION: 412
                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 337,194
FILING DATE: 12-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 496,236
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Murphy, Lisabeth Feix REGISTRATION NUMBER: 31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 393-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.9%;
Best Local Similarity 21.6%;
Matches 68; Conservative 36
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 340817 MACPAG SFO INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3031 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2398 AASGAGAAQEDALAP 2412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 RGLGWGLLPETQAAP 242
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969 VRSPQLHGAPLGGTPTLSPPLCSPNGYLGSLKPGVQGKKVRKPSSKGLACGSKEAKDLKA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GPVGRRRVSIVP--SAEGF------GEAIRRGLGWGLLPETQAAPMLKA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 VLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGAT-LTLRLEDEAHTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  909 NREETPLFLAAWEGSYETAKVLLDHFANWDITDHMDRLPRDIAQERMHHDIVRLLDEYNL 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DGKLDWAAMPVLRFG------PKDVLQDR---DLDGRVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1.5; 44; Mismatches 106; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 85; DB 1; Length 1068; 21.6%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1152...2219
OTHER INFORMATION: Highly conserved ankyrin repeat
OTHER INFORMATION: region of No. 5780300ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 SLLRRGDVLGAVTREANPVAGCEVV-ELG-TMRHLAIATPSLRDAYMV-
                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NAME: US/08/537,210A
FILING DATE: 29-SEP-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-027
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-969-9864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Artavanis-Tsakonas, Spyridon
       : Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1029 WRKKSQDGKGCLLDSSGMLSPVDS 1052
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Sequence 2, Application US/09113825

Patent No. 6149902

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Human N1 (TAN-1)
                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.8%
Best Local Similarity 21.6%
Matches 70; Conservative
                                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                  IX: USA
10036/2711
                      STREET: ALL
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       ADDRESSEE:
                                                                         STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
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TITLE OF INVENTION: Expression of Polypeptides and Its Use in the Preparation of TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GMLLVDQAR-TVLREVKVLKEMASQQGETMSGPLHIGL---IPTVGPYLLPHIIPMLHQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :|| || || :|| || 179-KLEMYLHEAQTHQLLAQLDSGKLDCVILALVKESERFIEVPLFDEPMLLAIYEDHP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GEVLVQAARKWVLLQAETKAQLSGRLAEI - - - PLTIAINADSLSTWFPPVFNEVASWGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 TLTLRLE---DEAHTLSLLRRGD-----VLGAVTREA---------NP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 VAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDRDL----DGR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------DLAGEKLLMLEDGHCLRDQAMGFCFEAG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08537210A
Patent No. 5780300
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mark
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 VDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 ADEDTHFRATSL----ETLRNMVAAGSGITLLPALAVPPERKRDGVVYL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 85.5; DB 1; Length 2; Pred. No. 0.18; A4; Mismatches 113; Indels
                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01120.0002-01000
                                                                                                                                             : 1300 I Street, N.W., Suite 700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/952,817
FILING DATE: 19920928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MSYETS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0112/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                         ZIP: 20005-22.COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~wenter: IBM PC compatible
~~~compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.8%;
Matches 63; Conservative 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 WANRECVPMA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-07-952-817-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 199209:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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1029 WRKKSQDGKGCLLDSSGMLSPVDS 1052

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Fortini, Mark

APPLICANT:

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APPLICANT: Diederich, AUGUELANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Martsuno, Kenji
TITLE OF INVENTION: DELIES, PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
TITLE OF ENHENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1948 -LLEASADANIQDNMGRTPLHAAVSADAQGVF-----QILIWNRATDLDARMHDGTTPL 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2060 NREETPLFLAAWEGSYETAKVLLDHFANWDITDHMDRLPRDIAQERMHHDIVRLLDEYNL 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 VLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGAT-LTLRLEDEAHTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001 ILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAAAVNNV-DAAVVLLKNGANKDMQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GPVGRRRVSIVP--SAEGF-----GEAIRRGLGWGLLPETQAAPMLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PKDVLQDR----DLDGRVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 SLLRRGDVLGAVTREANPVAGCEVV-ELG-TMRHLAIATPSLRDAYMV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 85; DB 1; Length 2556; 11.6%; Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 106;
                                                                                                                                 GENERAL INFORMATION: APPLICANT: Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                 E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                      ; Sequence 17, Application US/08185432 ; Patent No. 5750652
                                                                                                                                                                              Busseau, Isabelle
Diederich, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 735
TELECOMMUNICATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-8864/97.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                New York
                                           RESULT 15
US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 VLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGAT-LTLRLEDEAHTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               850 ILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAAAVNNV-DAAVVLLKNGANKDMQN 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              909 NREETPLFLAAWEGSYETAKVLLDHFANWDITDHMDRLPRDIAQERMHHDIVRLLDEYNL 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GPVGRRRVSIVP--SAEGF------GEAIRRGLGWGLLPETQAAPMLKA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLLRRGDVLGAVTREANPVAGCEVV-ELG.TMRHLAIATPSLRDAYMV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PKDVLQDR---DLDGRVD----
                    MANÍPULATION OF NON-TERMINALLY DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Mismatches 106; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1068; 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 AVISDFIYQGASL----HNQTDRTGETALHLAAR--YSRSDAAKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1152...2219
CHER INFORMATION: Highly conserved ankyrin repeat
CHER INFORMATION: region of No. 6149902ch
US-09-113-825-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.8%; Score 85; Best Local Similarity 21.6%; Pred. No. 1 Matches 70; Conservative 44; Mismatch
                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATINE: FRASEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7326-027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DGKLDWAAMPVLRFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/537,210
FILING DATE: 29-58P-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GEVILLDE----IPIDT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 735
TELECOMMUNICATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-869-8864
TELEFAX: 6141 PENNIE
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1068 amino acids
  Matsuno, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
APPLICANT: Matsuno,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1068 aminc
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                       STATE: N
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Search completed: September 13, 2001, 17:52:12 Job time: 1118 sec

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4.5
Compugen Ltd
GenCore version
Copyright (c) 1993 - 2000
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sw model - protein search, using OM protein

; Search time 25.14 Seconds September 13, 2001, 17:52:41 Run on:

(without alignments) 878.704 Million cell updates/sec

US-09-105-1171-3

1460 1 MNPIQLDTLLSIIDEGSFEG......RSLARLTDAVVDAAIEGLRP 290 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

	æ				SUMMAKIES		
Score	Query	y h Length		DB	ID	Description	
538.5	36.9		303	7	G70756	hypothetical prote	
410	28.1		300	~	B83100		
376.5	25.8		266	~	S22098	replication intiti	-
376.5	25.8		160	7	F85947	٦	
361.5		8	86	~	C82318	c	
177	12.	1 2	163	7	G83145	probable transcrip	
175	12.0		300	7	D83502		
174	11		95	7	E83302	probable transcrip	
170	11.6		110	~	E83381	probable transcrip	
163.5	11.2		98	7	A83482	probable transcrip	
156	10.7		104	7	E83495		
152.5	10.4		363	~	G83332		
152.5	10.4		36	7	D82443	0	
151	10.		102	7	B82036	ption	
149.5	10.2		33	~	C83290	probable transcrip	
149	10.2		103	7	G83354 ·		
4	10.		601	7	S70535		
143.5	٠		63	~	D86063		
143.5	•		902	7	F85823		
142.5		8	105	7	D64963		
141.5			111	7	H83174	probable transcrip	
140.5	•		105	7	B47099		
140	•	9	112	~	E83624	probable transcrip	
139.5			163	Н	RGECIY	regulatory protein	
139	•		601	~	D64139	metR protein homol	
138.5	6	5	105	7	G82167	transcription acti	
138.5			901	~	135595	probable transcrip	
			80	~	H65014	hypothetical prote	
138	о О		293	7	H70067		

probable transcrip	probable transcrip	probable transcrip	probable transcrip	probable LysR-like	transcription regu	probable transcrip	probable transcrip	probable transcrip	probable transcrip	trans-activator of	regulator for metE	lysR-type transcri	hypothetical prote	transcription regu	probable transcrip
F83023	C83536	C83310	C81954	E85517	H81011	B83536	E83498	B83158	D83319	A36066	D86070	T34997	F85869	A82436	D83630
7	7	7	~	7	7	7	7	7	7	7	7	7	~	7	7
294	298	309	309	299	309	314	296	317	298	317	317	292	312	313	302
9.3	9.3	9.5	9.1	0.6	0.6	9.0	8.9	8.9	8.9	8.9	8.9	8.8	8.8	8.8	8.8
136	136	135	133	131.5	131	131	130	130	129.5	129.5	129.5	129	128.5	128.5	128
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Н	
ULT	7756

RESULT 1

G70756
hypothetical protein Rv1985c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
C;Accession: G70756
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Telle: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-303 <Colb.
A;Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; FIDN:CAA98410.1; PID:g32615
A;Gene: Rv1985c
C;Superfamily: conserved hypothetical protein H11364

5 Gaps ., 6 Length 303; Query Match 36.9%; Score 538.5; DB 2; Length Best Local Similarity 43.1%; Pred. No. 7.8e-36; Matches 124; Conservative 49; Mismatches 106; Indels

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65 QAARKMVLLQAETKAQLSGR--LAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122 δλ

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EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWA 182

123

183 A--MPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240

Ω

241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288 Ω

inhibitor of chromosome initiation IciA PA4363 [imported] - Pseudomonas aeruginosa (s

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A; Map position: 62.8 min C; Function:
                                                                                       A; Molecule type: protein
                                1-297 <THO>
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                A; Molecule type: DNA
JN0079
                                                                                                                                                                                                                                                                                                                                      A; Gene: iciA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: iciA
                                                                                                                                                                                                                                                                                                                      C; Genetics
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K.; Lim,
                                                                                                                    A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
                                                                                                                                                   A;Accession: B83100
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-300 <STO>
A;Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07751.1; GSPDB:GN001
C;Genetics:
A;Gene: iciA; PA4363
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                                                   Hickey, Larbig,
                                                                                                                                                                                                                                                                                                                                                                      5
            C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83100 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replication intitiation inhibitor iciA - Escherichia coli
N;Alternate names: chromosome replication initiation inhibitor A
C;Species: Escherichia coli
A;Variety: strain K12-38
A;Variety: strain K12-38
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Mar-2000
C;Accession: S22098; S37499; JN0079; PS0203; C65076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AARKMVLLQAETK---AQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVQQVRLLEGDLQRWVPNLDEGGAPERLRIALNADSLATWWAAAVGDFCAERRVLLDLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDG--KLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 WAAMPVLRFGPKDVLQDRDL-DGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 LAGVPAIVFGPDDLLQHRFLKDLGVEGGFIHH --- LCPSSEGFVRLTAGGLGWGLVPERQ 245
                                                                                                                                                                                                                                                                                                                                                                      10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LAALAAVVEOGGFERAAQALGLSOSAVSORIKLLEARVGOPVLVRETPPHPTDLGRRLLN 68
                                                                                                                                                                                                                                                                                                                                   Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 VQGELARGELVELLPGQVIDVPLYWHYWRNGGELLASLTEHLLARAGDGL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AAPMLKAGEVI-LLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                               Query Match 28.1%; Score 410; DB 2; La
Best Local Similarity 36.9%; Pred. No. 1.5e-25;
Matches 107; Conservative 47; Mismatches 126;
                                                                                                                                                                                                                                                                                                                    Score 410; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Pseudomonas aeruginosa
                                                                                  /, S.; Olson, M.V.
406, 959-964, 2000
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A;Molecule type: DNA A;Residues: 1-297 <BLAT> A;Cross-references: GB:AR000375; GB:U00096; NID:91789282; PIDN:AAC75953.1; PID:917892 A;Experimental source: strain K-12, substrain MG1655 D.J.; May K.; Apoda A; Description: binds to the origin (oriC) of Escherichia coli DNA to block initiation A;Molecule type: DNA A;Residues: 1-297 <STO> ZCross-references: GRAE005174; NID:g12517445; PIDN:AAG58042.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933 A; Residues: 1-28, ^xx', 30-35, ^xx', 37-38, ^xxx', 41 < TH2>
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MuID:97426617
A; Accession: C65076 3; A; Status: preliminary; nucleic acid sequence not shown; translation not shown R; Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551 C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: F85947 66 AARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125 126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM- 184 185 -PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243 189 APVVAFDHLDDMHQAFLQQNFDLPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKE 248 Gaps 6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65 A;Cross-references: GB:M62865; NID:g146435; PIDN:AAA62780.1; PID:g146436 A;Accession: PS0203 hypothetical protein iciA [imported] - Escherichia coli (strain 0157:H7) 15; 244 LKAGEVILLDEIPIDTP-----MYWQRWRLESRSLARLTDAVVDAAIEGLR 289 Length 297; Indels Query Match 25.8%; Score 376.5; DB 2; Best Local Similarity 34.1%; Pred. No. 7.3e-23; Matches 100; Conservative 53; Mismatches 125; C;Superfamily: regulatory protein ampR C;Keywords: DNA binding; DNA replication inhibitor F;21-40/Region: helix-turn-helix motif

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A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross-references: GB:AE004817; GB:AE004091; NID:g9950181; PIDN:AAG07382.1; GSPDB:GN
A;Experimental source: strain PAO1
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X.; L
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A; Cross-references: GB:AE004544; GB:AE004091; NID:g9947060; PIDN:AAG04530.1; GSPDB:GN
                                                                probable transcription regulator PA3995 [imported] - Pseudomonas aeruginosa (strain C) Species: Pseudomonas aeruginosa (c) Species: Pseudomonas aeruginosa (c) Species: Pseudomonas aeruginosa (c) Species: Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (C) Accession: G93145 R: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A:Reference number: A82950; MUID:20437337
A:Accession: G83145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 -TPSL-RDAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFG 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 -GGATLTLRLEDEAHT----LSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.1%; Score 177; DB 2; Length 297
Best Local Similarity 28.0%; Pred. No. 7.1e-07;
Matches 78; Conservative 38; Mismatches 119; Indels
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C, Superfamily: hypothetical protein b1875
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C, Genetics:
A, Gene: PAI1
C, Superfamily: hypothetical protein b1875
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A; Status: preliminary
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-298 < HEL>
A; Cross-references: GB: AE004134; GB: AE003852; NID: 99654900; PIDN: AAF93655.1; GSPDB: GN001
A; Experimental source: serogroup 01; strain N16961; blotype El Tor
C; Genetics
A; Genetics
A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                  126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPFTQAAPM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 APVVAFDHLDDMHQAFLQQNFDLPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:: |:: | :| ;| ;| ;| || || || || || || ;| || 69 LYRRYCLIEQELVPELTNQEHVRPVSMSIATNADSLATWLLPALDKVMKSRQVELNLVIY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 IKAPAVSYDQYDELHNKFLWDYFAVPRDKVINHTVG-----SSEAFVRLALSGAAYC 240
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                                                                                                                                                                                                                  6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
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        Length 297;
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; Score 376.5; DB 2;
; Pred. No. 7.3e-23;
53; Mismatches 125;
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; Pred. No. 1.2e-21;
65; Mismatches 116;
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1 Similarity 29.9%;
86; Conservative 65
25.8%;
ilarity 34.1%;
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Match

Query

Qy 266 WRLESRSLARLTDAVV 281 Db 274 LKNQPLRKAAQELV 287	ulator PA2123 [imported] - Pseu uginosa snce_revision 15-Sep-2000 #text_ ; Erwin, A.L.; Mizoguchi, S.D.;	L.L.; Coulter, S.N.; Folger, N.K.; Mas, A.; Larbig, K.; Uence of Pseudomonas aeruginosa PA01, an opportunistic p MUID:20437337	A;Cross-references: GB:AE004639; GB:AE004091; NID:g9948129; PIDN:AAG05511.1; GSPDB:GN A;Experimental source: strain PA01 C;Genetics: A;Gene: PA2123 C;Superfamily: conserved hypothetical protein HI1364	Ouery Match 11.6%; Score 170; DB 2; Length 310; Best Local Similarity 25.7%; Pred. No. 2.78-06; Matches 77; Conservative 37; Mismatches 98; Indels 88; Gaps 12; Qy 5 QLDTLISTIDEGEREASLAISISPSAVQRVRALEHHVGRVLVSRTQPARATEAGEVLV 64 1:	66 EHACKLLQELEQAEASVLDADDDLRGQLRLSAPLAFTPRYLAPLLARFAERHPQLRVDVQ 1 96 ADS-LSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVV 1 1126 ADDRPVNLQEPRFDWALRMG	QY 204 VDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDEIPIDTP 260	RESULT 10 A83482 probable transcription regulator PA1309 [imported] - Pseudomonas aeruginosa (strain P C.Species: pseudomonas aeruginosa C.Species: Species: Sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C.Accession: A83482 R.Stover, C.K.; Pham, X.D.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;	er, S.N.; Folger, N.K.; Nas, A.; Latbly, N.; eudomonas aeruginosa PAO1, an opportunistic p 37	A,Residues: 1-286 <sto> A,Cross-references: GB:AE004560, GB:AE004091; NID:g9947240; PIDN:AAG04698.1; GSPDB:GN A,Experimental source: strain PAO1 C;Genetics:</sto>
Best Local Similarity 27.2%; Pred. No. 1e-06; Matches 82; Conservative 44; Mismatches 121; Indels 54; Gaps 12; Qy 6 LDFLLSIIDEGSFEGASLALSISPSAVSORVKALEHHYGRVLVSR-TQPAKATEAGEVLV 64	65 77 71 114	171 DAXWUDGKLDWAAMPULREGPKDVLQDRDLDGRVDGPVGRR-RVSIVPSA-EGEGEAIRR 171 DAXWUDGKLDWAAMPVLREGPKDVLQDRDLDGRVDGPVGRR-RVSIVPSA-EGEGEAIRR 180 NPCIDLDPLPIVTFPPRGVYRD-EMIAALEA-VGRRWHISFTSSSLGGLGSAIAD 229 GLGWGL	Oy 277 T 277 1 Db 292 T 292	RESULT 8 B83302 Cybbable transcription regulator PA2758 [imported] - Pseudomonas aeruginosa (strain PA01 C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: E833302 C;Accession: E833302 C;Accession: Exp. No.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000	A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A; Reference number: A82950; MUID:20437337 A; Recession: B83302 A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Rosidues: 1.295 <sto> A; Cross-references: GB:AE004703; GB:AE004091; NID:g9948825; PIDN:AAG06146.1; GSPDB:GN001 A; Experimental source: strain PA01 C; Genetics: A; Gene: PA2758</sto>	Query Match 11.9%; Score 174; DB 2; Length 295; Best Local Similarity 25.3%; Pred. No. 1.2e-06; Matches 80; Conservative 48; Mismatches 112; Indels 76; Gaps 15;	Qy 6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEVLV 64 :: ::	QY 108 NEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGT 158	SWGLLPETQ :: SWGNFPLSR

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127 NMEVFNGSWEAIAQGRADIVIGATA--AVPVGGDFEVRDMGILDWAFVMSPNHPCVREQN 184
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SRTRL 313
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Nature 406, 477-483, 2000

A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035, MUID:20406833

A; Accession: B82036

A; Residues: preliminary

A; Residues: 1-302 < HEIP

A; Residues: 1-302 < HEIP

A; Residues: GB:AE004342; GB:AE003852; NID:99657358; PIDN:AAF95899.1; GSPDB:GN001

A; Experimental source: serogroup 01; strain N16961; biotype El Tor

C; Genetics:
A; Gene: VC2760

A; Map position: 1
C; Superfamily: probable transcription regulator vbbS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription regulator LysR family VC2760 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Accession: B82036
                                                                                                                                                                                                                                                        ATEAGEVLVQAARKMVLLQAETK----AQLSGRLAEIPLTIAINADSLSTWFPP---VFN 108
                                                                                                                                                                                                                                                                                    FTEAGKLILERGR--AILAATEKLVNDATLLANGWELDITIALDG-----IVPAANLFP 112
                                                                                                                                                                                                                                                                                                                            EVASWGGATLT-LRLEDE--AHTLSLLR--RGDVLGAVTREANPVAGCEVVELGTMRHLA 163
                                                                                                                                                                                                                                                                                                                                                   --LRDAY----MVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLEDEAHTLSLLRRGD----VLGAVTREANPVAG-CEVVELGIMRHLAIATPS---LRDAY 173
                                                                                                                                              Gaps
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                                                                                                                                                                              1 MNPIQLDTLLSIID----EGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAK 55
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                                                                                                                                                                                                     PVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL---DEIPIDTPMYW
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                                                                                                          Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 151; DB 2; Length 302
26.1%; Pred. No. 8.8e-05;
.ive 53; Mismatches 118; Indels
                                                                                                                                              Indels
                                                                                                                       Best Local Similarity 25.5%; Pred. No. 6.4e-05;
Matches 79; Conservative 62; Mismatches 102;
                                                                                                          DB 2;
             A;Gene: VCA0575
A;Map position: 2
C;Superfamily: probable transcription regulator ybbs
                                                                                                      10.4%; Score 152.5; DB 325.5%; Pred. No. 6.4e-05;
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Best Local Similarity 26.19
Matches 69; Conservative
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273 RRNQMGEAKS 282
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C; Genetics
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Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Louson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: C83290
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription regulator PA2848 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: C83290 R;Stover, C.K.; Pham, X.O.: Erwin, A.T. Mishamonki et al. Mishamonki
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174 MVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 PSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL---DEIPIDTP--MYWQRWRLESR
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C;Superfamily: conserved hypothetical protein HIl364
                                                                                                      185 LSEGFIS-QFLAICLDDTSSVLPKRHTE-
                                                                                                                                                                                                                                                                                                                                                              :| | | :| :| | | | | | 239 YMPRHMAQPLLASGQLVEKVLPDE 262
                                                                                                                                                                                                                                                                       234 LLPETQAAPMLKAG---EVILLDE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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us-09-105-117i-3.rpr

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us-09-105-117i-3.rsp 83(6476)

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OM protein - protein search, using sw model

September 13, 2001, 17:57:09 Run on:

; Search time 15.26 Seconds (without alignments) 650.989 Million cell updates/sec

US-09-105-1171-3 1460 1 MNPIQLDTLLSIIDEGSFEG......RSLARLTDAVVDAAIEGLRP 290 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ပ	72 mycobacteri	94 escherichia	99 edwardsiell	•	89 klebsiella	-		-		-	84 salmonella					_	-						•	18 pseudomonas	_	95 rhodospiril	_	50 escherichia		m	CI.	83 mycobacteri
	Desc	P9463	010872	P241	052399	P70773	P52689	047005	008597	P05827	P45349	P77500	P05984	P52691	P19797	P10086	P52667	P52678	P36771	P33651	P52693	. P42722	P526	P51205	P375	P34818	001610	P52595	P52677	P76250	P42507	P7733	P7770	05068
SUMMARIES	ID	LYSG_CORGL	YJ85_MYCTU	ICIA_ECOLI	ICIA_EDWIC	ICIA_AERSA	LTRA_KLEPN	NAC_ECOLI	NAC_KLEAE	ILVY_ECOLI	METR_HAEIN	YFER_ECOLI	METR_SALTY	LRRA_SYNP7	METR_ECOLI	TFDR_ALCEU	ESTR_ACICA	OXYR_MYCLE	LRHA_ECOLI	BLAA_STRCI	NTCB_SYNP7	CFXR_ALCEU	PECT_ERWCH	YC30_PORPU	YDHB_ECOLI	TRPI_PSESY	OPRR_PSEAE	CBBR_RHORU	OXYR_MYCAV	YEAT_ECOL1	HVRB_RHOCA	YCJZ_ECOLI		YM82_MYCTU
	DB	П	-	Н			Н		-				٦	Н	.	-	-							-					Н	П	Н	-	, - 1	-
	Query Match Length	290	303	297	297	299	309	305	302	297	309	308	317	294	317	295	301	311	312	326	309	317	316	317	310	298	306	298	311	307	292	299	308	312
dР	Ouery Match	100.0	36.9	25.8	25.0	24.3	10.1	9.8	9.6	٠	٠		9.3		8.9				8.7	٠.	•			9.6	•							7.6	7.4	7 . 4
	Score	1460	538.5	376.5	365.5	355.5	148			139.5	139	138.5	136.5	136	129.5	128	127.5	127.5	127.5	127.5	126.5	126.5	126	125.5	121	117.5	116.5	115.5	115.5	111.5	111	111	108.5	108
	Result No.	н	7	m	4	2	φ	7	80	σ ;	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P42623 escherichia P74422 synechocyst P4421 haemophilus P55576 rhizobium s P52669 agrobacteri O34827 bacillus su O35038 bacillus su O35038 bacillus su P52690 rhodobacter P52655 enterobacte P27111 escherichia
YHAJ_ECOLI NTCB_SYNY3 ILLYY_HABIN YAMQ_RHISN TUA4_AGRVI YKUM_BAGSU CLCR_PSEPU YWFK_BACSU YWFK_BACSU CBBR_RHOSH BUDR_ENTAE
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298 309 292 298 304 294 299 310 143
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107.5 107.5 107 107 106.5 106.5 106.5 106.5 106.5
33 33 33 33 34 34 34 34 34 34 34 34 34 3

ALIGNMENTS

or send an email to license@isb-sib.ch). EMBL, X964T1; CAA6323.1; EMBL, X964T1; CAA6323.1; InterPro; IPR000847; PROSITE; PS00044; HTH_LYSR_FAMILY; 1. DNA-binding; Transcription regulation. SEQUENCE 290 AA; 31388 MW; 9CEOA63F775FCB74 CRC64;	
	entities or send creent; EMBL; XG InterPro Pfam; Pl PROSITE ONA-bind SEQUENCI
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	61 EVI 11
MNPIQLDTLLSTIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG MNPIQLDTLLSTIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG EVLVQAARKMVLLQAETKAQLSGRLAEIPLTTAINADSLSTWFPPVFNEVASWGGATLTL	121 RLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLD 180

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RESULT 2 YJ85_MYCTU

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                                                                              EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWA 182
                                                                                                                                                                              A--MPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240
                                                                                                                                                                                                                                           AAKAPSLAWNRDDGLQDM-LVRKAFRRAITRPTHFVPTTEGFTAAARAGLGWGMFPEKLA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOVE-Jensen B., Maigaard M.;
"Escherichia coli rpiA gene encoding ribose phosphate isomerase A.";
J. Bacteriol. 175:5628-5635(1993).
-1- FUNCTION: SPECIFIC INHIBITOR OF CHROMOSOMAL INITIATION OF
REPLICATION IN VITRO. BINDS THE THREE 13-MERS IN THE ORIGIN
(ORIC) TO BLOCK INITIATION OF REPLICATION.
-1- SUBUNIT: BEHAVES AS HOMODIMER IN SOLUTION.
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-41.
STRAIN=K12 / W3110;
MEDLINE=91239508; PubMed=2034653;
Thoeny B., Hwang D.S., Fradkin L., Kornberg A.;
"icia, an Escherichia coli gene encoding a specific inhibitor of chromosomal initiation of replication in vitro.";
Proc. Natl. Acad. Sci. U.S.A. 88:4066-4070(1991).
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SYRAIN=KIZ / MGIG55;
MEDLINE=97426617: Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
May B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CHROMOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR)
                                                                                                                                                                                                                                                                                                                  241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy I., Leadlay P.F.; Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      246 ASPLADGSFVRVCDIHLDVPLYWQCWKLDSPIIARITD-TVRAAASGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
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                                                                                                              240
181 WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 QLAALAAVVELGSFDAAAERLHVTPSAVSQRIKSLEQQVGQVLVVREKPCRATTAGIPLL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 QLDTILSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Taylor K., Whitehead S., Barrell B.G.; Squres S., Sqares R., Sulston J.: Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; Mature 393:537-544(1998).
                                                                                                          WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA
                                                                                                                                           SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 303;
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PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding.
Transcription regulation; DNA-binding.
13 42 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                  241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGLRP 290
                                                                                                                                                                                                                                           241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGLRP 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR RV1985C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE-98295987; Pubmed-9634230;
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Pfam; PF00126; HTH_1
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EMBL; M62865; AAA62780.1; -.

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Query Match Local

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EMBL; AF037440; AAB92569.1;
InterPro; IPR000847; -.
Pfam; PF00126; HTH_1; 1.
                                                                                                                           Similarity 33.4% 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, (Rel. 35, (Rel. 35, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aeromonas salmonicida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=NCIMB 1102;
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01-NOV-1997
01-NOV-1997
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P70773;
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ICIA_AERSA
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                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                 189 APVVAFDHLDDMHQAFLQQNFDLPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKE 248
                                                                                                                                                                                                                                                                         66 AARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125
                                                                                                                                                                                                                                                                                                69 LLRQVELLEEEWLGDEQTGSTPLLLSLAVNADSLATWLLPALAPVLADSPIRLNLQVEDE 128
                                                                                                                                                                                                                                                                                                                      126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM- 184
                                                                                                                                                                                                                                                                                                                                                                    185 -PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                              6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                             249 LASGELIDL-----TPGLFQRRMLYWHRFAPESRMMRKVTDALLDYGHKVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                244 LKAGEVILLDEIPIDTP-----MYWQRWRLESRSLARLTDAVVDAAIEGLR 289
                                                                                                                                                                                  Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHROWOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR)
                                                                                                    PRINTS; PRO0039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY; 1.
DNA-binding; Transcription regulation.
DNA_BIND 40 40
SEQUENCE 297 AA; 33471 MW; BAD60B76661E3EF CRC64;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                  25.8%; Score 376.5; DB 1; 34.1%; Pred. No. 3.5e-23;
                                                                                                                                                                                                         53; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 AA.
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             U28377; AAAOSUUST.,
AEO00375; AAC75953.1;
                                   X73026; CAA51508.1;
                                                                                                                                                                                              Best Local Similarity 34.1%
Matches 100; Conservative
                                          PIR: JN0079; JN0079.
PIR: S22088; S22098.
EcoGene; EC10490; IciA.
InterPro; IPR000847; -
Pfam: PF00126; HTH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwardsiella ictalur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=67780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=93-146;
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052399;
                                                                                                                                                                                   Query Match
                                   EMBL;
                          EMBL;
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                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 LLHQVELLEEEWLGNDNSSDGPLLLSLAVNADSLATWLLPALKPVLADSPLRLNLQVEDE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 MPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243
                                                                                                                                                                                                                                                                                                                                                                                                                               66 AARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDG--KLDWAA 183
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                   6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 APAVAFDHLDDMHQAFLQQNFELPPGSVPCHIVNSSEAFVQLALQGTTCCMLPHLQVERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CHROMOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 LKAGEVILLDEIPIDTP-----MYWQRWRLESRSLARLTDAVVDAAIEGLR
                                                                                       H-T-H MOTIF (BY SIMILARITY).
93BEC456B2419989 CRC64;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                    25.0%; Score 365.5; DB 1; 33.4%; Pred. No. 2.6e-22; ive 51; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 AA
PRINTS; PRO0039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
DNA-binding; Transcription regulation.
DNA_BIND 21 40 H-T-H MOI
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PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY;
                                                                                                                  297 AA; 33392 MW;
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48; Gaps

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MEDLINE-98155143; PubMed-9495755;
Muse W.B., Bender R.A.;
"The nac (nitrogen assimilation control) gene from Escherichia coli.";
J. Bacteriol. 180:1166-1173(1998).
                                                                                                                                                                                                              QHAQQMLEAARQAMDSAGSRQTVAQGKLTLSVPKAVGRFVIHPLMMAFFHRYPQVDVCLR 128
                                                                                                                                                                                                                                                                LEDEAHTLSLLRRG-DYLGAVTREANPYAGCEVVELGTMRHLAIATPSLRDAYMVDGKLD 180
                                                                                                                                                                                                                                                                                                             LED--RPLDFIDDGIDLALRITDTPSP--GLHGKPLMPIRHVICAT----EAY----LQ 175
                                                                                                                                                                                                                                                                                                                                                                  WAAMPVLRFGPKDV------LQDRDLDGRVDGPVGRRRVSIVPSAEGFG------ 223
                                                                                                                                                                                                                                                                                                                                                                                                  QHGTP---YTPQDLRAHSCISLGETPADARWK----FRREGKTETVQTYGRYAANHTAVR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 -EAIRRGLGWGLLPETQAAPMLKAGEVI-LLDE---IPIDTPMYWQRWRLESRSLARLTD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 LDAVRQHLGIGSLPLFTAREALANGDIVQVLPEWEFISSYSGDLWLLWAGDKHMPARMR- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RES. 3:3/9-324(1990).
FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE HUT, PUT AND URE
OPERONS AND REPRESSOR FOR THE GDH AND GLTB OPERONS IN RESPONSE TO
                                                                                                                                                              QAARKMV--LLQAETKAQLSGRLAEIPLTIAI-NADSLSTWFPPVFNEVASWGGATLTLR 121
                                                                                       LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NITROGEN ASSIMILATION REGULATORY PROTEIN NAC (NITROGEN ASSIMILATION
CONTROL PROTEIN).
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STRAIN=KIZ. / MG1657.
STRAIN=KIZ. / MG1657.
STRAIN=KIZ. / MG167.
SIRAIN=FIZ. / MG167.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Grab B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97251358; Pubmed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Mola C., Panamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Mola C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
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          Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AA
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       50;
             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 AMID 291
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          80;
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          Matches
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 RQLELE----LAGEIAPDEPQAPIRVSIAVNADSLATWFLPALAPLLEQHPIELNLLVDD 129
                                                                                                                                                                                                                                                                                                                                          71 VLLQAETKAQLSGRL-----AEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLED 124
                                                                                                                                                                                                                                                                                                                                                                                                                                               EAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM 184
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                      11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                   14 AVMQEQNFERAAQRLHITQSAISQRIKQLEQQFAEPLLIRSQPLQATPLGQKLLAHYRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Klebsiella
                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 PMLKAGEVILLDEIP---IDTPMYWQRWRLESRSLARLTDAVVDAAIEGLRP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 QQLAQG--ILLDLSPSHHLIEPLYWHRWVLERGLHKQISQRLISEGRRALQP 298
                                                                                                                                      Length 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bott M., Meyer M., Dimroth P.; "Regulation of anaerobic citrate metabolism in Klebsiella
                                                                                                                                                                                         Indels
DNA-binding; Transcription regulation.

DNA_BIND 21 40 H-T-H MOTIF (POTENTIAL).

SFOUENCE 299 AA; 33410 MW; 5EEBECA44CC5A68D CRC64;
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5C54D416605C734A CRC64;
                                                                                                                                    Query Match 24.3%; Score 355.5; DB 1; Best Local Similarity 33.6%; Pred. No. 1.7e-21; Matches 98; Conservative 49; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 148; DB 1;
Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR LIRA.
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PROSITE; PS00044; HTH_LYSR_FAMILY: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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309 AA; 34357 MW;
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26.3%;
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Best Local Similarity
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P52689;
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SEQUENCE
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LTRA_KLEPN
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                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 TPSLR-DAYMVDGK-----LDWAAMPVLR-FGPKDVLQDRDLDGRVDGPVGRRVSI-- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 QPLLKEDLYLVGTRDCPGQSVDLTAVAEMNLFLPRDYSAVR---ARVTEAFTLRRLSAKI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GEVLVQAARKMVLLQAE------TKAQLSGRLAEIPLTIAINADSLSTWFPPVF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 NEVASWGGATLTLRLEDEAHTL - SLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE HUT, PUT AND URE OPERONS AND REPRESSOR FOR THE GDH AND GLTB OPERONS IN RESPONSE NITROGEN LIMITATION. NEGATIVE REGULATOR OF ITS OWN EXPRESSION. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation; DNA-binding; Activator; Repressor;
Nitrate assimilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-T-H MOTIF (POTENTIAL).
775F219AF32AFADC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.6%; SCOIC 28.1%; Pred. No. 0.00020, 28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 IGEIESITTLTAAIASGMGATVLPESAARSLCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTIONAL ACTIVATOR PROTEIN ILVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
Bacteriol. 175:2107-2115(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86111952; PubMed-3003115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AA; 32754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L01114; AAA18173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.69
Best Local Similarity 28.19
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00039; HTHLYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00126; HTH_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B47099; B47099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. (
(Rel. (
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                                                                                                                                                 REGULATORS.
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01-NOV-1988
01-NOV-1997
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P05827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
NITROGEN LIMITATION. NEGATIVE REGULATOR OF ITS OWN EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKILYTHAR-AILRQCE-QAQLAVHNVGQALSGQVSIGFAPGTAASSITMPLLQAVRAE- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FPEIVIYLHENSGAVLNEKLIN--HQLDM-----AVIYEHSPVAGVSSQALLK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------C--EVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVINQAARKMVLLQAETKAQ-----LSGRLA------EIPLTIAINADS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-ROY-1997 (Rel. 35, Last annotation update)
NITROGEN ASSIMILATION REGULATORY PROTEIN NAC (NITROGEN ASSIMILATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLDGRVDGPVGRRRVSIVPSAEGFGE------AIRRGLGWGLLPETQAAPMLKA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDLFLVGTODCPGOSVDVNAIAOMNLFLPS------DYSAIRL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                        SIMILARITY).
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schwacha A., Bender R.A.; "The nac (nitrogen assimilation control) gene from Klebsiella aerogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGHTS: PRO0039; HTH.LYSR.
PROSITE; PS00044; HTH.LYSR.PAMILY: 1.
Transcription regulation; DNA-binding; Activator; Repressor;
Nitrate assimilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-T-H MOTIF (POTENTIAL).
B0B5DC408C6C6821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 142.5; DB 1;
25.3%; Pred. No. 0.00019;
iive 45; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AA
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STRAIN=W70 / KC1043;
MEDLINE-93209957; Pubmed=8458853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 AA; 32835 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 AE000290; AAC75050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90837; BAA15806.1;
EcoGene; EG14265; nac.
InterPro; IPR000847; -.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U56736; AAD14869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klebsiella aerogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=28451;
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                                                                                      REGULATORS.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Haemophilus
                                         METR_HAEIN
P45349;
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SEQUENCE
                            METR_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAARKMVLLQAETK-----AQLSGRLAEIPLTIAINADSLSTWFPPVFNEV-ASWGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 VFAQQTLLQYQQLRHTIDQQGPSLSGE-----LHIFCSVTAAYSHLPPILDRFRAEHPSV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 TLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA--TPSL----R 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 EIKLTTGDAADAMEKVVTGEADLAIAGKPETLPG--AVAFSMLENLAVVLIAPALPCPVR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQVSVE-KPDWSTVPF-----IMADQ-----GPV-RRIELWFRRNKISNPMIYAT 222
                                                                 Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region
from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                                                                                                     "The complete nucleotide sequence of the ilvGMEDA operon of Escherichia coll K-12.";
Nucleic Acids Res. 15:2137-2155(1987).

-!- FUNCTION: THIS PROTEIN ACTIVATES THE TRANSCRIPTION OF THE ILVC GENE IN THE PRESENCE OF ACETOLACTATE OR ACETOHYDROXYBUTYRATE.

-ILVY IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION.

-!- SUBCELLULAR LOCATION: CYTOPLASHIC.

-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 DAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00044; HTH_LYSR_PAMILY; 1.
Branched-chain amino acid biosynthesis; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 297;
                                                                                                                                                               MEDLINE-87174741; PubMed=3550695;
Lawther R.P., Wek R.C., Lopes J.M., Pereira R., Taillon B.E.
Hatfield G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROJATE,
Branchd-chain amino actu projetti Activator; Repressor; DNA-binding.

Activator; Repressor; DNA-binding.

NA BIND 18 37 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPSAEGFGEAIRRGLGWGLLPET--QAAPMLKAGEVILLDEIPIDTP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGGHEAMVSMVALGCGVALLPEVVLENSPEPVRNRVMILERSDEKTP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.6%; Score 139.5; DB 1
23.3%; Préd. No. 0.00032;
ative 50; Mismatches 115
Biol. Chem. 261:2441-2450(1986)
                         SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-92358234; PubMed-1379743;
                                                                                                                                     SEQUENCE OF 264-297 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M11689; AAA24028.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M32253; AAA24025.1; -. PIR; B26287; RGECIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M87049; AAA67576.1; -. AE000453; AAC77493.1;
                                                                                           from 84.5 to 86.5 minutes. Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EcoGene; EG10503; 11vY.
InterPro; IPR000847; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00126; HTH_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S30671; S30671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 67; Conserv
                                                                                                                                                                                                                                                                                                                    REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M87049;
                                                                                                                                                     STRAIN-K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 QAARKMY--LLQAETKAQLSGRLAEI-----PLTIAINADSLSTWFPPVFNEVAS-WGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATLILRLEDEAHT----LSLLRRGDVLGAVIREA-----NPVAGCEVVELGIMRHLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).
-!- FUNCTION: CONTROL OF THE LAST STEP IN METHIONINE BIOSYNTHESIS;
METR IS A POSITIVE ACTIVATOR OF THE META, METE AND METH GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation; DNA-binding; Methionine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
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SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METR IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION
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309 AA; 35344 MW; A0C2F0277DE8B274 CRC64;
                                                                                                     Last sequence update)
Last annotation update)
Ä.
                                                                                                                                                                      TRANSCRIPTIONAL ACTIVATOR PROTEIN METR
                                                                 (Rel. 32, Created)
(Rel. 32, Last seq
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                                                                                                                                                                                                                                           Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                              METR OR HI1739
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                                                             01-NOV-1995
                                                                                                 01-NOV-1995
01-NOV-1995
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164 IATPSLRDAYMVDGKLD--WAAMPVLRFGPKDVLQDRDLDGRV---DGPVGRRRVSIVPS 218
                coli
                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-UL-1908 (Rel. 40, Last annotation update)
11-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein; Transcription regulation; DNA-binding. 20 39 H-T-H MOTIF (POTENTIAL). 308 AA; 33903 MW; 23B6A771E4AB8587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                      308 AA
                                                                       219 AEGFGEAIRRGLGWGLLPETQAAPMLKAGEVI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0039; HTHLYSR.
PROSITE; PS00044; HTH LYSR.FAMILY; 1.
Hypothetical protein; Transcription ry
BONA_BIND 20 39 H-T-H MOY
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
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MEDLINE-97349980; PubMed-9205837;
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EcoGene, EG14159; yfeR.
InterPro, IPR000847; -.
                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        coli
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Gaps

63;

Query Match 9.5%; Score 138.5; DB 1; Length 308; Best Local Similarity 25.1%; Pred. No. 0.0004; Matches 78; Conservative 51; Mismatches 119; Indels 63.

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                                                                                                                                                                                                                                                                                                                      221 GFGE-----AIRRGLGWGLLPETQAAPMLKAGEVILLDEIPIDTPMYWQRW---RLESR 271
                                                                      64 VQAARKMVLLQAETKA-----QLSGRLAEIPLTIAINADSLSTWFPP--VFNEVA 111
                                                                                                                                               112 SWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAG--CEVVELGTMRHLAIATPSL 169
                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87307964; PubMed-3040668; Plamann L.S., Stauffer G.V.; "Nucleotide sequence of the Salmonella typhimurium metR gene and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Urbanowski M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CONTROL OF THE LAST STEP IN METHIONINE BIOSYNTHESIS;
METR IS A POSITIVE ACTIVATOR OF THE META, METE AND METH GENES.

METR IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL

REGULATORS.
               ----RD-AYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGR--VDGPVGRR--RVSIVPSAE
                                                                                                                                                                                                                                               169 LLCHRDSALAVEDYVPWQALQ----GAKLVLQDYASGSRPLIDAALARNGIQANIV---Q
QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG-RVLVSRTQPAKATEAGEVL
                                                                                                            -QLALRLERLLDELNSTLRDTGRMGQQLSGKVR-----VAASQTISAHLIPQCIAESHR
                                                                                                                                                                                  118 RYPDIQFVLHDRPQQWVMESIRQGDVDFGIVIDPGPVGDLQCEAI-----LSEPFF
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InterPro: IFR000847; -.
Pfam; PF00126; HTH 1; 1.
PRINTS; PR00039; HTHLYSR.
PROSTED: PSROGG44; HTH_LYSR.FRAMILY; 1.
Aranscription regulation; DNA-binding; Methionine biosynthesis; Activator; Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRANSCRIPTIONAL ACTIVATOR PROTEIN METR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                             272 SLARLTDAVVD 282
                                                                                                                                                                                                                                                                                                                                                                                                                 277 SLSTAAEALWD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            QAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVF-NEVASW------GG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                          QLANQ-VLPQISRALQACNEPQQTRLRIAIECHSCIQWLTPALENFRASWPQVEMDFTSG 125
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                                                                                                                                                                                                                                                       6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG-RVLVSRTQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96281517; PubMed-8661945; Anandan S.S.; Anandan S., Nalty M.S., Cogdell D.E., Golden S.S.; "Identification of two classes of transcriptional regulator genes the cyanobacterium Synechococcus sp. strain PCC 7942.";
                                                                                                                                                                                                                                                                                           -----YELGTMRHL---AIATPSLRDA-----YMVDGKLDWAAMPVLRFGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 SETLLIYPVQRSRLDVWRHFLQPAGISPLLKSVDNTLLLIQMVAARMGIAALPHW----
                                                                                                                                                                                         81;
                                                                                                                               Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arch. Microbiol. 166:58-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 DVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-T-H MOTIF (BY SIMILARITY).
90CD503F84BE8CC4 CRC64;
                                                                                                                                                                                            Indels
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PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation; DNA-binding.
Transcription 18 37 H-T-H MOTIF (POTENTIAL).
THE PS738747F149E335 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cus sp. (strain PCC 7942) (Anacystis nidular Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                               DB 1;
                                                                                                                                                                                         29; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV----
                                                                                                                           9.3%; Score 136.5; DB 23.9%; Pred. No. 0.0006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-6CT-1996 (Rel. 34, Created)
01-6CT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR LRRA.
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38 H-
35585 MW;
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                                                                                                                                                         Best Local Similarity 23.9%
Matches 69; Conservative
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19
317 AA;
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DNA_BIND
SEQUENCE
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12;

Gaps

94;

Indels

87;

42; Mismatches

Conservative

Query Match Best Local Similarity Matches 68; Conserv

9.3%; Score 136; DB 1; Length 294; 23.4%; Pred. No. 0.00061;

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                                                                                                                                                                                                                                                                                                            -----AGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPK 192
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STRAIN=KIZ / MG1655,
STRAIN=KIZ / MG1655,
DANIELS D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
DANIELS D.L., Plunkett G. III, Burland P.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region Efrom 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=8909836; PubMed=2643109;
MEDLINE=89098936; PubMed=2643109;
MAXON M.E., Redfield B., Cal X.-Y., Shoeman R., Fujita K., Fisher W.,
Stauffer G., Weissbach H., Brot N.;
"Regulation of methionine synthesis in Escherichia coli: effect of
the Metr protein on the expression of the mete and metr genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:85-89(1989).
-i. FUNCTION: COMTROL OF THE LAST STEP IN METHIONINE BIOSYNTHESIS;
METR IS A POSITIVE ACTIVATOR OF THE META, METE AND METH GENES.
METR IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS
HOMOCYSTEINE AS AN INDUCER.
-i. SUBCELLULAR LOCATION: CYTOPLASMIC.
-i. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
61 GERVLOLAQRMLQLHDSIVHEVNLEKGLQGGHLRIASFRSAATHVLPPRLALFRQRCP--
                                                                                                                                                                                                                                                             ---ANPV---
                                                                                                          GEVLVQAARKMVLLQAET - - KAQLSGRLAEIPLTIAINADSLSTWFPP - - - VFNEVASWG
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"Structure-function studies on Escherichia coli MetR protein, a
putative prokaryotic leucine zipper protein.";
proc. Natl. Acad. Sci. U.S.A. 87:7076-7079(1990).
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01-NOV-1997 (Rel. 35, Last annotation update)
TRANSCRIPTIONAL ACTIVATOR PROTEIN METR.
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01-FEB-1991 (Rel. 17, Last seq
01-NOV-1997 (Rel. 35, Last anno
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P19797;
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eutrophus JMP134
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"Analysis of duplicated gene sequences associated with tfdR and tfdS
in Allyanes eutrophus JMP134 ";
J. Bacteriol. 176:2348-2353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG-RVLVSRTQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 SETLLIYPVQRSRLDVWRHFLQPAGVSPSLKSVDNTLLLIQMVAARWGIAALPHW----
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                                                                                                                                                                                                 PIR; S30718; S30718.

BEOGGANE; EG10591; metR.

Interpro; IPR000847; -.

PRINTS; PR000339; HTHLL1/1.

PROSTTE; PS000044; HTHLLYSR FAMILY; 1.

Transcription regulation; DNA-binding; Methionine biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 129.5; DB 1; Length 317; 23.3%; Pred. No. 0.0022; tive 33; Mismatches 111; Indels 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H-T-H MOTIF (BY SIMILARITY).
L -> T (IN REF. 3).
513F5C710803800D CRC64;
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01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
TRANSCRIPTIONAL REGULATORY PROTEIN TDFR/JFDS.
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Alcaligenes eutrophus (Ralstonia eutropha).
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317 AA; 35629 MW;
                            M37630; AAA62781.1; -. M87049; AAA67624.1; -. AE000458; AAC76831.1; -. J04155; AAA24159.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator; Repressor.
DNA_BIND 19 3
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PIR; S30718; S30718
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64 VQAARKMVLLQA----ETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNE-VASWGGATL 118
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                                                                                                                                                                                                                                                                                                                                                                    ARE IDENTICAL. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; TRR00047; -.
Pfam; PF00126; HTH 1; 1.
PRINTS; PR00039; HTHLIVSR.
PROSTIE: PS00044; HTHLIVSR.PAMILY; 1.
Aromatic hydrocarbons catabolism; Transcription regulation;
DNA-binding; Activator; Repressor; Plasmid.
18 37
EEQUENCE 295 AA; 32070 MW; C6C477BE8127A41R CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8%; Score 128; DB 1; Length 295; 24.4%; Pred. No. 0.0027;
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Matches 76; Conservative
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pseudomonas
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vibrio chol
                             bacillus su
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                                                                   salmonella
                                                rhizobium
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The Set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces colloclor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

SMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

REMEL; A1357613; CAB93745.1; -.

REMEL; PRO00126; HTH.LYSR.

R Pfam; PF00126; HTH.LYSR.

R PROSITE; PS002126; MTTCH_CARRIER; UNKNOWN_1.

R PROSITE; PS00215; MTCH_CARRIER; UNKNOWN_1.

R PROSITE; PS00215; MTCH_CARRIER; UNKNOWN_1.

R PROSITE; S00215; MTCH_CARRIER; UNKNOWN_1.

R PROSITE; S00215; MTCH_CARRIER; UNKNOWN_1.

SEQUENCE 300 AA; 32205 MW; 7122FE5A539D642B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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         09krd6
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Q9hy39
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE LYSR-FAMILY TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                      ALIGNMENTS
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                                              052827
091568
0916N2
0910F7
066393
09RDH0
09L3R4
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09F186
09JXG8
09I569
09I4F4
09HXB8
09I0N6
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          Q9KRD6
086805
P96725
Q9HUH6
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MEDLINE=97000351; PubMed=8843436;
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(without alignments)
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                                                                                                                        1 MNPIQLDTLLSIIDEGSFEG.....RSLARLTDAVVDAAIEGLRP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                      425026 seqs, 132305027 residues
                                                                 September 13, 2001, 17:56:48
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Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Q87968

Q9HW38

Q9HX36

Q914J4

Q91085

Q911Z2

Q911Z2

Q911A35

Q914D7

Q91Q75

Q91Q77
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Q9L6S5
Q67999
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sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_noertebrate:*
sp_mmmmal:*
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sp_vertebrate:*
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Maximum DB seq length: 200000000
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1460
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sp_rodent:*
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Match Length DB
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Perfect score:
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                                                                                                                    RLARQVARLERDASAELGLRGEGEPTRVTVAVNADSLATWFLPALTRIPREPALCFELRR 131
                                                                                                                                          EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL--D 180
                                                                                                                                                     EAGEVLVQAARKMVLLQAETKAQL - - SGRLAEIPLTIAINADSLSTWFPPVFNEVASWGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 ATLTLRLEDEAHTL------SLLRRGD-VLGAVTREANPVAGCEVVELGTMR 160
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                                                                 12 QVRTLLAVVDEGTFDAAAAALHVTPSAVSQRVKALEQRTGRVLLLRTKPVRATDSGAVLV 71
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                                                     QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLV
                                                                                                                                                                                    WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                             Umeyama T.;
"Open reading frame encoded around afsA gene.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL; AB011413; BAA32133.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.4%; Score 472.5; DB 2; Length 303; 39.3%; Pred. No. 1.7e-28; tive 49; Mismatches 93; Indels 51;
          Length 300;
                                                                                                                                                                                                                                             241 APMLKAGEVI-LLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: irnoull.

Pfam: PF00126; HTH_1: i.
PR.NTS: PR00129; HTH_LYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY; UNKNOWN_1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
DNA-binding: Transcription regulation.
ana aa: 31866 MW; F1D146DD95aa0CE3 CRC64;
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                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
          DB 2;
                    1.6e-37
        40.4%; Score 590.5;
llarity 44.5%; Pred. No. 1.6e
Conservative 51; Mismatches
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InterPro; IPR001993;
                   Similarity
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01-NOV-1998 (
01-MAR-2001 (
                              129;
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         Query Match
Best Local (
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                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 AARKMVLLQAETK---AQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                  69 HVQQVRLLEGDLQRWVPNLDEGGAPERLRIALNADSLATWWAAAVGDFCAERRVLLDLVV
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                                                                                                RVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVI-LLDEIPIDTPMYWQRWRLES
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36.9%; Pred. No. 1e-23;
ive 47; Mismatches 126; Indels
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PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE 300 AA; 32451 MW; BFC7F298E51CFBE9 CRC64;
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Last annotation update)
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1-MAR-2001 (TrEMBLrel. 16, Last sequence
01-MAR-2001 (TrEMBLrel. 16, Last annotation INHIBITOR OF CHROMOSOME INITIATION ICIA.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PAO1;
MEDLINE=20437337; Pubmed=10984043;
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Nature 406.959-964(2000).
EMBL: AEO04852; AAG07751.1;
Interpro; IPR000847; -.
                                                                                                                                                                                                                              271 RSLARLTDAVVDAAIEGL 288
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280 PALAAVAEAVAAEAAEAL 297
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PROBABLE TRANSCRIPTIONAL REGULATOR
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EMBL, AE004544; AAG04530.1;
InterPro; IPR000847; -.
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nes 78; Conservative
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Best Local S
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STRAINEL TOR NIG661 / SEROTYPE 01;
MEDLINE-EL TOR NIG661 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AARKMVLLQAETKAQLSGR--LAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 DEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                               Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M--PVLRFGPKDVLQDRDL------DGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000).
-!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS
EMBL; AE004134; AAF93655.1; -.
TIGR; VC0482; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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PRINTS: PR00039; HTH_LYSR.
PROSTE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
DNA-binding: Transcription regulation.
SEQUENCE 298 AA; 33653 MW; C7776C56A9FD2521 CRC64;
                                                             Last sequence update)
Last annotation update)
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR.
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298 AA
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PRT;
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                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
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PRELIMINARY;
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Best Local Similarity
Matches 86; Conserv
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NCBI_TaxID=287;
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                  D9KUN3;
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74 LYAYARNIVELEREARARLHGTPIRDRLRIGASEDFASAWLPRVLQRFRRWHPEASIELK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 PEPCVYREAAIT--ALGAAARPW-----RLVFESASMAGCLSAALAGFAVTVVARSQ--- 243
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MEDLINE=20431337; PubMed=10984043;
MEDLINE=20431337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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STRAIN-PAO:
MEDLINE=20437337; PubMed=10984043;
StOVEC.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
StOVEC.K., Pham X.O.T. Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
"Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 -GGATLTLRLEDEAHT----LSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 -TPSL-RDAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen.";
Nature 406.959-964(2000).
Nature 406.959-964(2000).
InterPro: IPR000847; -.
Pfam: PF00126; HTH_11: 1.
PROSTE: PS00144; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE 297 AA; 32515 WW; 3809B555D453B720 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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NCBI_TaxID=287;
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                                                                                                                                                                                                      180 NPC----IDLDPLPIVTFPPRGVYRD-EMIAALEA-VGRRWHISFTSSSLSGLOSAIAD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Ras A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                       114 GGATLTLRLEDEAHTLSLLRRGDVLGAVTREAN---PVAGCEVVELGTMRHLAIATPSLR 170
                                                                                                                                                                                                                                                              137 MSRDLSASYDRGELDLVILKQ----RRASREALACWPEKTCWV-------DSAR 179
                                                                                                                                                                                                                                                                                       DAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRR-RVSIVPSA-EGFGEAIRR 228
                                                                                                                                                                                                                                                                                                                                        229 GLGWGL-------LPETQAAPMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARL 276
                                                                                                                                                                                       65 QAARKMVLLQAETKAQLSGRLAEIPLTIAINAD------SLSTWFPPVFNEVASW 113
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                       6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                               54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                     Length 300;
                                                                                    12.0%; Score 175; DB 2; Length 30 27.2%; Pred. No. 9.6e-06; Live 44; Mismatches 121; Indels
          Pfam; PF00126; HTH_1; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
SEQUENCE 300 AA; 32670 MW; A56BD8C9BD07B67B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTH_LYSR_FAMILY; UNKNOWN_1.
; 31890 MW; 8F46BFB7356EAOAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR.
PA2758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-PAO1;
MEDLINE-20437337; PubMed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:595-964(2000).
EMBL; AE004703; AAG06146.1; -.
InterPro; IPR000847; -.
                                                                                     Query Match
Best Local Similarity 27.23
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
 IPR001066;
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PROSITE; PS00044; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                          277 T 277
                                                                                                                                                                                                                                                                                                                                                                                                                292 T 292
InterPro;
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Gaps

16;

11.9%; Score 174; DB 2; Length 295; 25.3%; Pred. No. 1.1e-05; tive 48; Mismatches 112; Indels

80; Conservative

Best Local Similarity Matches 80; Conserva

Query Match

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12;
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                                                                                                                                                                    NEVASWGGATLTLRLEDEAHTLSLLRRGDV---LGAVTREANP-----VAGCEVVELGT 158
                                                                                                                                                                                                                                                                              174 PRHPALQKPG-QALYL-------EELVNVRQILVASCDLPLADTRPLIAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S---AEGFG---EAIRRGLGWGLLPETQAAPMLKAGEVILLD-----EIPIDTPMYWQR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 ACWRTDSLGTALEMVEAGIGWGNFPLSRVAPLLATGRLVRLDFRNTKNELKLPVHAIW-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | ::: | | | | :: | | | | :: | EHACRILLGELEQAEASVLDADDDLRGQLRLSAPLAFTPRYLAPLLARFAERHPQLRVDVQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ADDRFVNLQEPRFDMALRMG-----RLDDSCLV-------------ARPIT---- 158
                                                                                                                                                                                                                                                                                                                                                                     159 MRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDRD-LDGRVDGPVGRRRVSIVP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS-LSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVV 154
LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEVLV 64
                                      5 QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: | :: | || |: | : | || || : | 6 EMTTFVSVVDAHSFSEAARRIGTTKSQVSQRIQQLERRLGRVLLNRTRPLSLTDPGRTYY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 AA; 34611 MW; 258E15C239BEFE7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                          QAARKMVLLQAETKAQLSGRLAEIP-----LTIAINAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 170; DB 2; 25.7%; Pred. No. 2.4e-05; vative 37; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 QAARKMV--LLQAET------KAQLSGRLAEIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004639; AAG05511.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 -- LKNOPLRKAAOELV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00039; HTHLYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00126; HTH_1; 1
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                           NCBI_TaxID=287;
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                                                                                 Pseudomonas
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                                                                       204 VDGEPASFRIRVRMRTDSGHQLLEGARAGLGLAILPSFLAADALLAGE--LLPVLPGYSP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20437337; PubMed=10984043; Stover C.K., Pham X.C.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.C.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an Opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LRLGNAQETLAALLSEHVDVAVLTEVEARPGLFLEELVNSRICALLPRQHPWCERNEGV- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 DWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRR------RVSI-VPSAEGFGEA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 -----PLEELDQQIMVLREPGSITRRTFDRACAEQGVQPRVLLELDSREAVTEA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA 59
                           ---ANRHLLCASP------DYLARHGVPQHPEELQAHDGLVYYNREPGGMLCLP
                                                        204 VDGPVGRRRVSI----VPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDEIPIDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
          ELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKD------VLQDRDLDGR--
                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%; Score 163.5; DB 2; 27.7%; Pred. No. 6.8e-05; tive 32; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 VAAELGVGVVSSLEVGNDPRVRAVPLV 255
                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 IRRGLGWGLL------PETQAAPML 244
                                                                                                                                         PRT;
                                                                                                                                                                                                      PROBABLE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004560; AAĞ04698.1; -.
InterPro; IPR000847; -.
                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 27.78
Matches 74; Conservative
                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                 PA1309.
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=287;
                                                                                                                                                                                                                                                     Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                        091435
091435;
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Q914D7;
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Stover C.K., Phan K.O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Gollry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 GGATLTLRLEDEAHTLSLLRRG-DVLGAVTR--EANPVAGCEVVELGTMRHLAIATPSLR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 PRLEVVLQLDD--RIVDFEKEGYDLAIRITRLQDSSLIAR----QLGTSRRVVCCSPEYL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 QAARKMVLLQ-----AETKA----QLSGRLAEI-PLTIAINADSLSTWFPPVFNE-VASW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG-RVLVSRTQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ъ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                             Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE 304 Aa; 33974 MW; 9AAZE242AE5CABBI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 EGFGEAIRRGLGWGLLPETQAAPMLKAGEVI--LLDEIPIDTPMY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 QTMRDAAVRGLGLAMLPLFIAAEDLAAGRLVEALPQERPLDDLIY 272
                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE FRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 156; DB 2; 26.7%; Pred. No. 0.00028;
                                                                                               PROBABLE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                     STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004550; AAG04590.1;
InterPro; IPR000847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.73
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
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16;

us-09-105-117i-3.rspt

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RESULT
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

MEDLINE-20406833; PubMed-10952301;

Meddelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Comportunistic pathogen. Feedunce of Pseudomonas aeruginosa PAO1, an Nature 406:959-964(2000).

BMBL, AEUO4677; AAGOS885.1; --
InterPro: IPR001066; --
InterPro: IPR001066; --
                                                                                                                                                                                                                                                                                                                                                                             LVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122
                                                                                                                                                                                                                                                                                                                                                                                                        65 LLGYARRLLRLSDEASEALSPAHGDGVLRLGVPEDLAGEVLMPVLTRFTE---ERPRLRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                      EDEA ----HTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGK 178
                                                                                                                                                                                                                                                                                                                     4 IQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQ-PAKATEAGEV 62
                                                                                                                                                                                                                                                                                                                                     216 LASLVAAVGAGLGVSLLPLGCVGPEHRLLGAQAGFPPIAGLELALYARPELDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            вастегіа; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_тахID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGWFGSAARPFGEGSPEEPVP----LVVFPVGALYRQEMIHALESIGRRWRIGYSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AIRRGLGWGLLP------ETQAA-PMLKAGEVILLDEIPIDTPMYWQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDW---AAMPVLRFGPKDVLQDRDLDGRVDGPVGR-RRVSIVPSAEGFGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                              DB 2; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVESGLSHHLLRLYRSGELDLLLVKQWGADSDC------HARWAEP----
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                      Pfan: PF00126; HTH 1; 1.
PRINTS: PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
SEQUENCE 292 AA; 32054 MW; 1B7E8AB9C4396CDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                           10.4%; Score 152.5; DB 2; 25.9%; Pred. No. 0.00049; Live 41; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPTIONAL REGULATOR, LYSR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| || | : || :||:
--AGRTLRDRLRD-LCDARLEGLQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 RLESRSLA-RLTDAVVDAAIEGLR 289
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.99
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholerae
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                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
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STRAIR=L TOW NIG961 / SEROTYPE 01;
MEDLINE=L1 TOW NIG961 / DENOTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Raad T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 ATEAGEVLVQAARKMVLLQAETK----AQLSGRLAEIPLTIAINADSLSTWFPP---VFN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVASWGGATLT-LRLEDE--AHTLSLLR--RGDVLGAVTREANPVAGCEVVELGTMRHLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 IATPS------LRDAY----MVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 PVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL---DEIPIDTPMYW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                          1 MNPIQLDTLLSIID----EGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 VAAPTHYVHRRSGEFNEEAREKYRAIAIADTAREQPAMSV-----NILQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHOLETAE., /
NATURE 406:477-483(2000).
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                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                       Length 295;
                                                                                                                                                                                                                                                          Indels
                     TIGR; VCAUS/2;
InterPro; IPR000847; -.
Pfam; PF00126; HTH_1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEEEB28511225CE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSCRIPTIONAL REGULATOR, LYSR FAMILY.
                                                                                                                                                                                                    Score 152.5; DB 2;
Pred. No. 0.0005;
2; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00126; HTH_1; 1.
PRINVS; PR00039; HTHLYSR.
DNA-binding; Transcription regulation.
SEQUENCE 302 AA; 34281 MW; DEEB28
                                                                                                                                                                                                       10.4%; Sco
25.5%; Pre
tive 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO THE LYSR EMBL; AE004342; AAF95899.1; TIGR; VC2760; -.
EMBL; AE004388; AAF96477.1;
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 QRWRL-ESRS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| :: |::|
273 RRNQMGEAKS 282
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
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64 VQAARKMYLLQAETKAQLSG--RLA-EIPLTIAINADSL-----STWFPP----- 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 DLSGRPDFRPAIECENGHSLLGVVLASDAIG--ISSGLG-----DLAPPGQGGLRPLR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 DLDGRVD-GPV----GRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAG-EVIL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-201;
MEDLINE-2047337; PubMed-10984043;
MEDLINE-2047337; PubMed-10984043;
MEDLINE-204 Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Felger K.R., Kas A., Larbig K., Lim R.M., Brizer J., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVL 63
                        ----LDWAAMP----VLRFGPKDVLQDRDLDGRVDGPVGRRRVSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VFNEVASWGGATLTLRLE-------DEAHTLSLL--RRGDVLGAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 VRYPKARVSFQVEHWQALNRRLQAEEFEFFVADTRHFEADPQYRTSRLRPRRWHF---CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 REANPVAGCEVVELGTMRHLAIAT----PSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDR
                                                                     198 YLREHGVPASPGELPEHAGIDWDNLSPPYAWRF *** -- OHDGKLOHLRPKRARLAT
                                                                                                                    PSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL---DEIPIDTP--MYWQRWRLESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 149; DB 2; Length 303;
24.9%; Pred. No. 0.00095;
Live 47; Mismatches 102; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00126; HTH_1; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY; UNKNOWN_1.
PROGENCE 303 AA; 33686 MW; FCE1C76FD4F47874 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 REGHPLAARESVSAEELLSFPLATNISPPNIRKVLV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 LDEIPIDTPMYWQRWRLESR---SLARLTDAVVD 282
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created 01-MAR-2001 (TrEMBLrel. 16, Last se 01-MAR-2001 (TrEMBLrel. 16, Last an probable TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004659; AAG05722.1;
InterPro; IPR000847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                        169 LRDAYMVDGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
                                                                                                                                                                                                                 272 SLARL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                 RESULT 15
Q911E4
                                                                                                                                                                                                                                                                                                                                                                                  Q911E4
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                                                                                                                                                                                                                                    68 LEARQLLRQMEEIRAQTKRAAHGWRKTLKVTLD-NVVKLDKMKPMVEAFYQTFDFAELQI 126
                                                                                                                                                                                                                                                                                                                  174 MYDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWG 233
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                                                                                                                                                                                                                                                                                      RLEDEAHTLSLLRRGD----VLGAVTREANPVAG-CEVVELGTMRHLAIATPS---LRDAY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 NPGLDVQLRLIGSFIDL----QGEHLGEVDLVLRAGPLPDSRLVATSLAPMVRVVCASPE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AGLAFADRARRIVTELRLARAEAVSLSTAPQGLIRIDAPVPFGRRHLA---PAVADFLKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 WGGATLTLRLEDEAHTLSLLRRGDVLGAV--TREANPVAGCEVV--ELGTMRHLAIATPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DTL-----LSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPA-KATE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
Length 302;
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PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE 339 AA; 37280 MW; BDFB5DE083D2F86D CRC64;
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Last annotation update)
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10.3%; Score 151; DB 2; L 26.1%; Pred. No. 0.00067; Live 53; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 LLPETQAAPMLKAG---EVILLDE 254
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EMBL; AE004711; AAG06236.1; -.
InterPro; IPR000847; -.
                                                 Conservative
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                      Best Local Similarity
Matches 69; Conserv
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